us-10-800-161-28.rge

OM nucleic -

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Searched:

Minimum 1 Maximum 1

Database

Sequence:

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AC146165 Pan trog1
AC147293 Pan trog1
AL1929356 Plasmodiu
BC058827 Homo sapi
AL1313166 Human DNA
BV208515 FYE 2226
AC130873 Rattus no
AC116290 Rattus no
AC131170 Rattus no
AC131170 Rattus no
AC131170 Rattus no
AC131170 Rattus no
AC1310614 Rattus no
AC1310614 Rattus no
AC1306176 Sequence
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AC1088573 Mouse DNA
AC0088677 Homo sapi
AC008127 Homo sapi
AC069107 Homo sapi
AC069307 Homo sapi
AC069307 Homo sapi
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AL157900 Homo sapi
AL358434 Human DNA
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1 (bases 1 to 1700)

Cad, R. M. and Dietrich, R. A.

Arabidopsis gene encoding a protein involved in the regulation of the spression in plants

Patent: US 6706952-A 3 16-MAR-2004;

Syngenta Participations AG; Basel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              578 ICTAAAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAATCTCCACCGTCCAATTTATTTAGTTGACAATATCGACCGTCTAAGTTCCACACC
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Pred. No. 1.4e-51;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                          1700 bp
Sequence 3 from patent US 6706952.
AR488147
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                                                                                                            AC130614
AC131425
BX085721
BX085721
AC008584
AC008427
AC008427
AC079257
AC063307
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AC0600084
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AC0600084
AC0600084

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BC058827
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BV208515
AC130873
AC116290
AC131170
AL935316
BX248236
CQ691076
AL645566
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                                                                                                                                                                                                                                                                                                                       AR488147.1 GI:47253921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.6%;
Matches 273; Conservative
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276137
174887
228572
                                                                                              192808
248748
263298
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203865
173409
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166348
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AK175239 Arabidops
AC008564 Homo sapi
AC010633 Homo sapi
AC073528 Homo sapi
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AB023041 Arabidops
CS007929 Sequence
CS025770 Sequence
AR488146 Sequence
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AC024628 Homo sapi
AC05158 Homo sapi
AC05158 Homo sapi
AX20879 Sequence
BC017775 Homo sapi
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Homo sapi
Homo sapi
                                                                       (without alignments)
6762.964 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                               time 2303 Seconds
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BX647196
BX647195
                                                                                                                 1 tctagaaatatagccgatac.....acgacgccgttaacattttc
             GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                                                               ; Search
                                                                                                                                                           5883141 segs, 28421725653 residues
                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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CS02770
CS025770
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AK175239
AC010633
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AX209879
BC017775
AX511499
HSM807340
HSM807339
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                                              nucleic search, using sw model
                                                              January 11, 2006, 23:58:55
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                                                                                                                                         Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 su
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DB seq length: 200000000
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9b_on: *
9b_on: *
9b_on: *
9b_br: *
9b_pr: *
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Perfect score:
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Direct Submission

Direct Submission

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Direct Submission

Institute, Department of Plant Gene Research; 1532-3, Yana, Kisaraau, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-394)

Address for correspondence: kaos@kazusa.or.jp

Por the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MPEII
Genes with similarity to proteins in the databases are described in protein similarity to proteins in the databases are described in protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail

(Informatics Group, Oak Ridge National Laboratory, http://compbio.orni.gov/Grail-13/),

GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html),

NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of SplicePredictor (Volker Brendel, Stanford University, http://www.cbs.dtu.dk/servicedbytRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/RNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis, This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.

The 5' clone is K9122 and the 3' clone is MJL14.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E. and Tabata, S. Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty
                                                                                                                                                                                                                                                     PLN 14-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
GACGCCTATAAGAGTTTCATTATAATTTTTAGCAAAATAAAATCAGCAAATAATTTTTC 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 83650)
Sato, S., Nakamura, Y., Kaneko, T., Kato, T., Asamizu, E. and Tabata, S.
Direct Submission
                                                                                                                                                                                             83650 bp DNA linear PLN 14-FBB-2
AB023041 BA000014
AB023041.1 GI:4220640
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3190. 3273,3410. 3514)
/note="gpl AAD55139.1
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/coctype="Columbia"
/cooplement(542. .764)
/note=="CDS is reported in Acc# AP000599
contains similarity to CHP-rich zinc finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
                                                    Arabidopsis thaliana (thale cress)
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DNA Res. 7 (2), 131-135 (2000)
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/number=1
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REFERENCE
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ETIEGAADAYATKKIEPALAAATGAASSVISNEGSSMIGASGSSIDLDKKIVUSTUT
QQAGESKKASFPFDFALAAATGAASSVISNEGSSMIGASGSSIDLDKKIVUSTUD
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join (21893. .22063,22330. .22386,22578. .22783,22894. .23227,
23311. .23382,23473. .23613)
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similar to unknown protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MVLEKKSALLEDLIKKCGGCAVVDGGFATQLEIHGAAINDPLWS
AVSLIKNPELIKRYHMEYLEAGADIVVTSSYQATIPGFLSRGLSIEBSBSLLQKSVEL
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TGPFGRITASDPPYTSGSPAPASGIAPPPPPYTAKATTTVILPPLLPDSSIVPFTA
MQSAVSKNMIESLSVPFFRVGYPVNTDALDALYEKVKPKGVTMTALLAKAAGMALAQH
                                                                                                                                                                                                                                                                                                          PŪVNASCKDCKSFSYNSSINIAVAVAINGGLITPVLQDADKIDLYLLSQKWKELVGKA
RSKQLQPHEYNSGTFTLSNLCMFGVDRFDAILPPGQCAIMAVGASKPTVVADKDGFFS
VKNTMLVNVTADHRIVYGADLAAFLQTFAKIIENPDSLTL"
complement (4594. .5106)
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/db_xref="01:9279592"
/tanalation="MNNSLKKEREVEEDNGKSDGNRGKPSTEVVRTVTEEVDEFFKI
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DPVSQDLDSVMKSFENELSTTTAALSSGETQPDLGYLFEASDDELGIPPPLTPPQTLL
PPSCEETVTELVRASSDSSEVGELGFEDHVTEFGPCDLGDDGLFEYFDGCLDSGDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mmeprakydrolmytiogtleeasicllncgpigsnalknivug
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fvvndpyatdyssseeeersgrrkkyvceidlppragaatgaesesycgesnnngvsk
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product="AP2_domain_transcription factor-like protein"
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/product="homocysteine S-methyltransferase AtHMT-1"
/protein_leaba01052.1"
/db xreff="GI:9279594"
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11923 GACGGCTATAAGAGTTTTCATTATAAATTTTTAGCAAAATAAAATCAGCAAATAATTTTTTC 11864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfitzner, A. and Roth, B. Chemically-inducible promoters for the expression of proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1027 ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT
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         TCTAGAAATATAGCCGATACCAATTTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                                                        GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTC
                                                                               CAATCTCCACCGTCCAATTTAATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
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99.6%; Pred. No. 2.2e-48;
iive 0; Mismatches 1
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Sequence 2 from Patent WO2005014829.
CS025770.1 GI:60496427
                                                                                                                                                                                                                                                              241 TTGACTAAAGCTTAAACGACGCCGTTAACATTTTC
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Universitaet Hohenheim (DE)
Location/Qualifiers
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Sequence 2 from Patent EP1502953.
CS007929
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Best Local Similarity 99.6
Matches 259; Conservative
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CS007929
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FTPPYVLSSSVGFAQIFYPESPNSELIRLAQEKNMKIALGILEKAKKICLMHGIKAET 
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36797. 36871) 
/note="unnamed protein product; contains similarity to 
transcription-associated zinc ribbon protein 
gene_id:MPEII.II"
                                                                                                                                                                                                                                                                                                                                                                                                                                            NEPTEMEDVDSDSTAVNLLGERASEITVVDLSDGERGEEEVEEVEEEEEVVVEEEEEGIV
TTEEDQERNKPQKLTCPLCRGHIKEWVVKAARCFMNSKHRSCSCETCDFSGSYSDLR
KHARLLHPGYRESEADPERQESWRRLERQSDLGDLLGTLQSSFGGDEISNDGFLFAD
TRLLTVYFLIRVFRPESSGSRSSSWSSTSRATHTSGRRRSSRPASLWGESYEGNTGT
SRDEENVOSSDEQVSGTRRRSRRTVIDDDDEEEEP
complement (join 32197. .32430, 32525. .32676, 32969. .33332,
33404. .33487))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trainlation="MATPLSISNPLTSRHCYRLHLSSTSFKGNVSVLGANPSQILSL
KLNQTLKTRNQQQPARPLVVSQTAATSSAVVAPERFRLDNLGPQPGSRKKQKRKGRG
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STQAKEKLEASGCTLTVLPGRKKWVKPSVAKNQARADEYFAKKRAAAARATSEPAAS
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QTTYYTCPNCAHRFTEG"
join(37285...37965,38579...38674)
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                                                                                                    /evidence=not_experimental
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/translation="MTHARBERSSLTTTLLMVILLSYMLHLFCVYSRVGAIRIFPETP
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VCMEHPHNGILLICSSYENGCRPYMCDTSHRHSNCFDQFRKASKEKPSLSLLREEEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (join(33961. .34021,34114. .34226,34391. .34482,34602. .34800))
/note="unnamed protein product; gb|AAF26483.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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complement (27277, .27552)
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Pred. No. 5.8e-52;
0; Mismatches 1; Indels
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similar to unknown protein"
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Best Local Simil
Matches 273; C
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12103 TCTAAAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA 12044

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61 ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120

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RAFL21-66-M11.
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                                                                                                                                                            SOURCE
ORGANISM
                                                                           DEFINITION
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JOURNAL
REFERENCE
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JOURNAL
                           RESULT 6
AK175239
LOCUS
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                                                                                                                                VERSION
KEYWORDS
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             Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                               61 ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120
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                                                                                                               Chemically-inducible promoters for the expression of proteins in
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                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
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                                                                                                                                              Patent: WO 2005014829-A 2 17-FEB-2005;
Universitaet Hohenheim (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               0; Mismatches
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AR488146
Arabidopsis thaliana (thale cress)
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/organism="unknown"
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                                                                                                Pfitzner, A. and Roth, B.
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Matches 259; Conservative
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An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1-E vector (Carninci et al. (2001) Genomics 77:79-90) digested with BamHI and Sall. This clone is in a modified pBluescript vector.

Please visit our web site (http://rarge.gsc.riken.jp/) for further
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Lrryhvatrtvakvnggvaegelpskkrkrsqnlglrnsldcngvrdgefdeinrvgl
Qglgldlncktepdsvslsl"
   PLN 09-SEP-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Totoki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K., Kobayama, M., Sakaki, Y., Sakurai, T., Iida, K., Kayama, Y., Satou, M., Toyoda, A., Sakaki, Y., Sakurai, T., Iida, K., Kawai, J., Hayashizaki, Y. and Shinozaki, K. Carninci, P., Direct Submission
Direct Submission
Submitted (16-SEP-2004) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:mseki@ge.riken.jp,
WRL:http://rarge.gsc.riken.jp/, Tel:81-45-503-9585,
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AK175239 544 bp mRNA linear PLN 09-
Arabidopsis thaliana mRNA for NIMIN-2, complete cds, clone
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18.2%; Score 50; DB 15; Length 544;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 50; Conservative 0; Mismatches 0; Indels

    . 544
    /organism="Arabidopsis thaliana"

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Arabidopsis thaliana
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/protein_id="BAD43002.1"
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db xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                            Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Submitted (28-ARR-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (Dases 1 to 14384)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (01-MAY-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
5 (Dases 1 to 14384)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (08-JUN-2001) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94599, USP,
On Jun 8, 2001 this sequence version replaced gi:13876485.
Draft Sequence Produced by DOB Joint Genome Institute
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                    AC008964 143841 bp DNA linear PRI 08-JUN-
fomo sapiens chromosome 5 clone CTD-2360A17, complete sequence.
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OB Joint Genome Institute and Stanford Human Genome Center.
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DOB Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Finishing Completed at Stanford Human Genome Center www-shgc. stanford.edu Quality: Phrap Quality >=40 99.9% of Sequence; Estimated Total Number of Errors is 0.1.
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/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2360A17"
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DOE Joint Genome Institute.
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RESULT

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Homo sapiens chromosome 12 clone RP11-148D15, WORKING DRAFT
PRI 31-JUL-2001
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DOB Joint Genome Institute and Stanford Human Genome Center.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (31-701-2001) DOE Joint Genome Institute, 2800 Mitchell
Brive, Walnut Creek, CA 94598, USA
On Jul 31, 2001 this sequence version replaced gi:13677000.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195931)
DOB Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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1 (bases 1 to 167034)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
AC010633 195931 bp DNA linear PRI 31-JUL.
Homo sapiens chromosome 5 clone CTD-2317K6, complete sequence.
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Best Local Similarity 56.3%; Pred. No. 1;
Matches 85; Conservative 0; Mismatches 66; Indels 0;
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Pinishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.4.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="CTD-2317K6"
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DOE Joint Genome Institute.
Direct Submission
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AC073652.15 GI:14547458
                                                                                        AC010633.8 GI:15042798
                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                      Homo sapiens
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Alabrooks, S. L., Amaratunge, H. C., Ner, J. R., Banks, T., Barbaria, J., Barcon, J. Binnes, K., Blumhanung, K., Momili, N., Paouk, J., Burken, M., Barnalli, K., Momili, N., Paouk, J., Burken, M., Barken, M., Bornalli, K., Momili, N., Paouk, J., Burken, M., Burken, M., Barken, M., Morati, M., Maria, C., Charago, C., Charago, C., Chang, C., Harris, C., Ha
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TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

NOTE: Betimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

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92852 ARTICALITITAACCAACIACACTALICAGIGIAALALGIGGCAGGAACALTIALAAAG 92911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC073528 16 TO041 bp DNA linear PRI 01-MAY-2001 Homo sapiens 12 BAC RP11-8P16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
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                                                                                                                                                                                                                                                                                           48 ATTCCAAAAGTCAATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATG 107
                                                                                                                                                                                                                                                                                                                                                      108 ATGTCATTAGCATCAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTC 167
                                                                                                                                                                                                                                                                                                                                                                                                                     168 TAAGTTCCACACCGACGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGC 227
                                                                                                                                                                                                                                                           0; Gaps
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                        Query Match
16.1%; Score 44.2; DB 14; Length 167034;
Best Local Similarity 51.2%; Pred. No. 2;
Matches 103; Conservative 0; Mismatches 98; Indels 0; C
                                                                1 167034: contig of 167034 bp in length.
Location/Qualifiers
                                                                                                              organism="Homo sapiens"
                                                                                                                               /mol_type="genomic_DN/
/db_xref="taxon:9606"
                                                                                                                                                                             /clone="RP11-148D15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92972 CATITCITITATITGITTA 92992
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Homo sapiens
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Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Miner, G., Miner, T., Mitchell, T., Mohabbat, K., Montgomer, Y. K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newtson, J., Newtson, N., Oguh, M., Okwuon, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuon, G., Oragunye, N., Orteo, R., Pace, A., Payon, B., Perez, J., Peterz, L., Pickens, R., Primus, E., Pul. L., Ouiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Saerry, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shooshtaria, N., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wall, R., Ward, S., Walliams, G., Warren, R., Wall, R.,
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AUTHORS
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(bases 1 to 167041)

Direct Submission
Submitted (22-UTM-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 167041)

REFERENCE AUTHORS TITLE JOURNAL

Submitted (01-MAY-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 1, 2001 this sequence version replaced gi:13876431.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email Direct Submission

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html

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complement (7612. .7923)
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      --------- Summary Statistics
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Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Talagaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

Lu bubmitted (01-MAR-2000) Whitehead Institute/MIT Center for Genome Steearch, 320 Charles Street, Cambridge, MA 02141, USA

On May 25, 2000 this sequence version replaced gi:7144995.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                             Insert size: 228000; agarose-fp
Insert size: 205676; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; sum-of-contigs
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 ATTCCAAAAGTCAATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 TAAGTTCCACACGGCGGCTATAAGAGTTTCATTATAAATTTTTAGCAAATAAAATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                         Length 167041;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 207976)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 12, clone RP11-632011
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                               98;
                                                                                                                                                                                                                                                                                                                                                                           DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                   /rpt_family="MIR"
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/rpt_family="L2"
11288. .11321
                                                                                                                                                                                                                                                                                           complement (12398. .12636)
/rpt_family="MLT1G"
complement (12641. .13107)
                                                                                                                                                                                                                                                                                                                                                                         Score 44.2;
Pred. No. 2;
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complement(82567.8962)
/rpt_family="L2"
89667.9036
                                                                                                                                                                                                  rpt_family="AT_rich" 1478. .12092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74069 CATTTCTTTTTTTTTAA 74049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC024628.3 GI:8076668
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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7924. .7941
                                                                                                                                                                                                                                                                             'rpt family="MLT1G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 AAATAATTTTTTTGACTAA 248
                                                                                                                                                                                                                                      /rpt_family="L2"
complement(12162.
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                                                                                                                                                                                                                                                                                                                                                                           16.1%;
                                                                                                                                                                                                                                                                                                                                                                                                               Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                 repeat_region
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TITLE
JOURNAL
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AC024628
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AUTHORS
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KEYWORDS
SOURCE
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셤 ð a ð 엄 ò

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721 65720: gap of 100 bp

731 76314: contig of 10594 bp in length

7315 88196: contig of 11782 bp in length

737 10265: contig of 13769 bp in length

7397 102665: contig of 13769 bp in length

7306 102165: contig of 13769 bp in length

7371 116470: gap of 100 bp

7371 135171: contig of 14205 bp in length

7381 1335171: contig of 17047 bp in length

7381 1335172: contig of 17047 bp in length

7389 0717893: contig of 17047 bp in length

7390 171889: contig of 100 bp

740 171889: contig of 100 bp

750 171889: contig of 36087 bp in length

750 171889: contig of 36087 bp in length.
of 10290 bp in length
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3722. .8821
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 contig
gap of J
contig
gap of J
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                                                                                                                                                                                                                                                                                                               /map="12
                                                                                                                                                                             133618
171790
171890
                                          76315
76415
88197
88297
102066
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Hominidae, Homo.

In (Dases I to 266344)

Ribbases I to 266344)

Hiller,L.W., Fulton,R.S., Fulton,L.A., Graves,T.A., Pepin,K.H., Ribbases I to 266344)

Hiller,L.W., Fulton,R.S., Fulton,L.A., Jaeger,S., Walker,R., Wajle,K., Sekhon,M., Becker,M.C., O'Laughilin,M.D., Schaller,M.E., Pewell,G.A., Delehaunty,K.D., Miner,T.L., Nash,W.E., Cordes,M., Du,H., Sun,H., Edwards,J., Bradshaw-Cordum,H., Ali,J., Andrews,S., Isak,A., Vanbrunt,A., Nguyen,C., Loue,H., Ali,J., Andrews,S., Kalicki,J., Ozersky,P., Blelicki,L., Scott,K., Holmes,A., Kalicki,J., Ozersky,P., Blelicki,L., Scott,K., Holmes,A., Rarkins,R., Harris,A., Strong,C.M., Hou,S., Tomlinson,C., Buphin-Kohlberg,S., Kozlowicz-Reilly,A., Leonard,S., Rohlfing,T., Buchin-Kohlberg,S., Wang,S.P., Miller,N., Johnson,D., Murray,J., Strowmatt,C., Latreille,P., Miller,N., Johnson,D., Murray,J., Woesener,J.P., Wendl,M.C., Yang,S.P., Schultz,B.R., Wellshow,J.W., Spieth,J., Bieri,T.A., Nelson,J.O., Berkowicz,N., Wohldmann,P.B., Cook, L.L., Hickenbotham,M.T., Eldred,J., Williams,D., Bedell,J.A., Mardis,B.R., Clifton,S.W., Chissoe,S.L., Marra,M.R., Raymond,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145680 GATAGTTCATCCCATGAAAAGAGAAATTGATCATGAAGAATTACTAAACTATAAAAAGT 145739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145560 AİTATACAAATATACACATAAGAAATTGAİTCTAAATAAGCAATATAACATCACATTTTG 145619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC005158 266344 bp DNA linear PRI 30-JAN-2004
Homo sapiens BAC clone GSI-250N6 from 7, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 ATTCCAAAAGTCAATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AIGICALTAGCALCAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 TAAGTTCCACACCGACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 51.2%; Pred. No. 1.9;
Matches 103; Conservative 0; Mismatches 98; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC005158.3 GI:13446342
                                                                               4813. .34912
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AC005158
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PUBMED REFERENCE AUTHORS

TITLE JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

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Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu
                                                                                                                                                               This clone is from the first BAC library from Genome Systems, Inc. (http://www.genomesystems.com).
Cell line: lymphoblastoid
Haplotypes: two
                                                                                                                                                                                                                                                                                                                                                                Actual start of this clone is at base position 1 of GS1-250N6 actual end is at base position 266344 of GS1-250N6. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3681...3865
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6297...6466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .266344
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23875. .24166
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9857. .20139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome="7"
                                                                                                                                                     SOURCE INFORMATION:
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Submitted (30-JAN-2004) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 25, 2001 this sequence version replaced gi:5091650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-JUN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
8 (bases 1 to 266344)
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (20-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-MAR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-JUN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
                            Bubb, K., Simms, E., Levy, R., Clendenning, J., Kaul, R., Kent, W.J., Lucky, T.S., Baertsech, R.A., Brent, M.R., Keibler, E., Flickek, P., Bork, P., Suyama, M., Balley, J.A., Portnoy, M.E., Torrents, D., Chinwalla, A.T., Gish, W.R., Eddy, S.R., McPherson, J.D., Olson, M.V., Ethler, E.B., Green, E.D., Waterston, R.H. and Wilson, R.K.
The DNA sequence of human chromosome 7
Nature 424 (6945), 157-164 (2003)
     Haugen, E., Gillett, W., Zhou, Y., James, R., Phelps, K., Iadanoto, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                        2 (bases 1 to 266344)
Bauer,C., McPherson,C. and Williams,D.
The sequence of Homo sapiens BAC clone GS1-250N6
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://genome.wustl.edu
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: H_GS250N06
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Submitted (30-SEP-2000)
University, 4444 Forest
6 (bases 1 to 266344)
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7 (bases 1 to 266344)
                                                                                                                                                                                                                                                                                                                               3 (bases 1 to 266344) Materston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 (bases 1 to 266344)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 (bases 1 to 266344)
Waterston, R.
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REFERENCE AUTHORS TITLE JOURNAL

JOURNAL

COMMENT

REFERENCE AUTHORS

TITLE JOURNAL

REFERENCE AUTHORS /rpt_family="Alu" 28192. .28253

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the

MAPPING INFORMATION:

/rpt_family="Alu" 25208. .25431

repeat_region repeat_region repeat_region

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Consensus quality: 88918 bases at least Q40
Consensus quality: 93000 bases at least Q30
Consensus quality: 93760 bases at least Q30
Consensus quality: 93760 bases at least Q30
Consensus quality: 93760 bases at least Q30
Estimated insert size: 94453; sum-of-contigs estimation
Cuality coverage: 6.12 in Q20 bases; pulse field gel estimation
Quality coverage: 6.12 in Q20 bases; pulse field gel estimation
Quality coverage: 6.12 in Q20 bases; pulse field gel estimation.
**NOTE: This is a 'working draft' sequence. It currently
**Consists of 7 contigs. Gaps between the contigs
** are represented as runs of N. The order of the pieces
** is believed to be correct as given, however the sizes
** of the gaps between them are based on estimates that have
** provided by the submittor.
** This sequence will be preserved.
** provided by the submittor.
** This sequence will be preserved.
** the accession number will be preserved.
** a 34594: contig of 15494 bp in length
** 51244 66425: contig of 15449 bp in length
** 51244 66425: contig of 15449 bp in length
** 51246 66425: gap of unknown length
** 7367 7326: gap of unknown length
** 7367 7326: gap of unknown length
** 7367 7329: gap of unknown length
** 7367 7329: contig of 5841 bp in length
** 7367 7329: gap of unknown length
** 73680 80779: gap of unknown length
** 79680 80779: gap of unknown length
** 80780 80779: gap of unknown length
** 10cation/Qualifiers
** Location/Qualifiers
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/estimated.length=unknown
51144. /estimeted.length=unknown
6426. .66525
/estimated.length=unknown
72367. .72466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /estimated length=unknown
80680. .80779
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                                                                                                                                                               Center Project Name: 391027, H433
Center clone name: CIT-HSPC_536A23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                     Web site: http://www.jgi.doe.gov
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DN/db_xref="taxon:9606"
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                                                                                                                                         Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162972 ATTICTTAAAAGGATTCCACAAAATGAAAACATAATAATCCGGCTTGAAAAACCTCATT 163031
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="unknown"
/protein_id="AAS02015.1"
/db_xref="G1:41393490"
/translat="G1:41393490"
/translat=on="MEAQSHSSTTTEKKKVENSIVKCSTRTDVSEKAVASSTTSNEDE
SPGOTYTRERRNAITMOPOWNGGLSKVSEEPSTSSDERASLIKKEIHGSLPHVAEPSV
PYRGTVFAMDPRNGYMEPHY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC008563 94703 bp DNA linear HTG 18-JUL-2000
Homo sapiens chromosome 5 clone CTC-536A23, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 CTTACGCTTTAAAACATCGCATGATGATGTCATTAGCATCAATCTCCACCGTCCAATTTA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On May 6, 2000 this sequence version replaced gi:7708951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 TITAGITGITGACAATATCGACCGICTAAGITCCACACCGACGGCTATAAGAGTITCATT 201
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 94703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 AATTITICCACACATGGACTICCTITATICCAAAAGICAATAAAGIGIGACGICAIGATA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                                      /note="Homo sapiens GLI-Kruppel family member GLI3 cephalopolysyndactyly syndrome) (GLI3), mRNA.;
                                                                                                                                                                                                                                       complement (join (<30701. .30943,105605. .105728))
/gene="GLI3"
                                                                                                                                                                                complement (join(30701. .30943,105605. .105771))
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This gene was based on gi(13518031)
Continues as H GS489L14.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.8%; Score 43.4; DB 8; Best Local Similarity 50.2%; Pred. No. 2.7; Matches 107; Conservative 0; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 ATAMATTTTAGCAMAATAMAATCAGCAMATAMT 234
                                                               /rpt_family="MIR"
30611. 30652
/rpt_family="(CA)n"
complement(30701. 105771)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34549. .34579
/rpt family="(TrTTG)n"
34931. .34953
/rpt family="(TCTCCC)n"
36317. .36368
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Sequencing of Human Chromosome 5
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28282. .28508
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HTG; HTGS PHASE2; HTGS DRAFT.
Homo sapiens (human)
Homo sapiens
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DOE Joint Genome Institute.
Direct Submission
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                                                                                                                                                                        gene="GLI3"
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Garcialano, N.A., Peters, G.J., Abzamson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Wulting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalbka, Schmutz, J., Mars, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Greeration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 36 Row: m Column: 7.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLLL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web Site: http://www.ahgo.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 GACTATAACAGAAATCATATTTAATATTAAAATTAATACTTCAAATATCTTTCACATT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Straubberg.R.
Direct Submission
Submission
Submitted (30-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 TCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGAC
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                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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24:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="Lung"
/clone lib="NIH MGC 77"
/lab host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:4692106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 504)
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                                                            72120 İTİTCTAAĞGTCAĞİTAAİTİTCAAİĞAATATACİTTİTCACCATİTACAATTTGAAAAC 72179
                                                                                                                                                                         72180 TGATAATGAAAATTCATTACAACCTTTCTGAACTCAACTGGGCAAGAATTATTTCATA 72239
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1 (Dasse I to 504)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buatow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heiseh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 GACTATAACAGAAATCATATTTAATATTTAAATTTAATACTTCAAATATCTTTCACATT 104
           TCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Algate, P.A. and Mannion, J. Compositions and methods for the therapy and diagnosis of ovarian
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                        184 GGCTATAAGAGTTTCATTATAAATTTTAGCAAATAAAATCAGCAAATAATTTTTTTGTTG
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Pred. No. 28;
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CORIXA CORPORATION (US)
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/db_xref="taxon:9606"
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Sequence 1719, Ap
Sequence 1719, Ap
Sequence 6, Appl
Sequence 22, Appl
Sequence 3602, Ap
Sequence 3602, A
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Sequence 24, Appl
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                                                                                 ; Search time 812 Seconds (without alignments) 2790.406 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO8A_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-800-161-27
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US-10-800-161-24
US-10-800-161-3
US-10-800-161-3
US-10-800-161-3
US-10-800-161-3
US-10-800-161-1
US-10-800-161-1
US-10-900-161-1
US-10-027-622-102510
US-10-027-632-102511
US-10-027-632-102511
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US-10-101-510-676
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US-10-101-510-542
US-10-242-535A-36002
US-10-085-783A-36002
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Maximum Match 100%
Listing first 45 summaries
                                                         using sw model
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Gapop 10.0 , Gapext 1.0
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Sequence 69, Appl
Sequence 2, Appli
Sequence 10963, A
Sequence 2117, Ap
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GENERAL INFORMATI
Sequence 534423,
Sequence 7701, Ap
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Sequence 585231,
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Sequence 147687,
Sequence 147688,
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14.4 375 3

14.2 6301 6

14.0 794 5

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| Sequence 28, Application US/10800161
| Publication No. US20040154051A1
| GENERAL INFORMATION:
| APPLICANT: Cade, Rebecca M
| APPLICANT: Lawton, Kay Ann
| TITLE OF INVENTION: INDUCIBLE PROMOTERS
| FILE REFRENCE: A-31089CIP|
| CURRENT FILING DATE: 2004-03-12
| PRIOR APPLICATION NUMBER: 60/171,008
| PRIOR APPLICATION NUMBER: 60/171,008
| PRIOR FILING DATE: 1999-12-15
| PRIOR APPLICATION NUMBER: 60/175,519
| PRIOR FILING DATE: 1999-12-15
| NUMBER OF SEQ ID NOS: 31
| SEQ ID NO 28
| LENGTH: 274 TYPE: DNA ORGANISM: Arabidopsis thaliana Query Match 100. Best Local Similarity 100. Matches 274; Conservative

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61 ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120
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                                                                                                                                                                                                    331 ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTTAGCAT
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                                                                                                                                                                        1 TCTAGAAATATAGCCGATACCAATTTTTCCACACACAGACTTCCTTTATTCCAAAAGTCA
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                                                                       Length 544;
                                                                                                                     1; Indels
                                                                    99.4%; Score 272.4; DB 7; 99.6%; Pred. No. 2.7e-60; iive 0; Mismatches 1;
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; Sequence 25, Application US/10800161
; Publication No. US20040154051A1
; GENERAL INFORMATION:
APPLICANT: Cade, Rebecca M
APPLICANT: Cade, Rebecca M
APPLICANT: Lawton, Kay Ann
TITLE OF INVENTION: INDUCIBLE PROMOTERS
FILE REFERENCE: A.31089G(TP1
; CURRENT APPLICATION NUMBER: US/10/800,161
; CURRENT PILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/171,008
PRIOR APPLICATION NUMBER: 60/171,008
PRIOR PILING DATE: 1999-12-15
; PRIOR PILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 25
LENGTH.: 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-800-161-25
, ORGANISM: Arabidopsis thaliana
US-10-800-161-27
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Matches 273; Conservative
                                                                                              Best Local Similarity 99.6
Matches 273; Conservative
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Pred. No. 2.1e-60;
0; Mismatches 1;
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  TIGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
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| Publication No. US20040154051A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Cade, Rebecca M
| APPLICANT: Dietrich, Robert A
| TITLE OF INVENTION: INDUCIBLE PROMOTERS
| FILE REPERENCE: A-31089CIP1
| CURRENT APPLICATION NUMBER: US/10/800,161
| CURRENT APPLICATION NUMBER: 60/171,008
| PRIOR PILING DATE: 1999-12-15
| PRIOR PILING DATE: 2004-01-11
| NUMBER OF SEQ ID NOS: 31
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 27
| TYPE: DNA
                                                                                                             SQUENCE 26, Application US/10800161
Publication No. US20040154051A1
GENERAL INFORMATION:
APPLICANT: Cade, Rebecca M
APPLICANT: Dietrich, Robert A
APPLICANT: Lawton, Kay Ann
TITLE REFERENCE: A-31089CIP1
CURRENT APPLICATION NUMBER: US/10/800,161
CURRENT PILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/171,008
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VET. 2.1
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; ORGANISM: Arabidopsis thaliana
US-10-800-161-26
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Best Local Similarity 99.6%;
Matches 273; Conservative
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NAME/KEY: misc_feature
) LOCATION: (863)...(1228)
) OTHER INFORMATION: NI16 genomic coding region
US-10-800-161-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (757)..(762)
OTHER INFORMATION: HEXAMERAT 4 element
                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (609)...(614)
OTHER INFORMATION: MYCATR22 element
                 ORGANISM: Arabidopsis thaliana
                                                        NAME/KEY: misc feature
LOCATION: (365)..(374)
OTHER INFORMATION: TCA1 motif
                                                                                                                                                                                  motif
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Best Local Similarity 99.65
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (707)..(712)
OTHER INFORMATION: PAL BOX
                                                                                                                                                               LOCATION: (426)..(435)
OTHER INFORMATION: TCA1
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NAME/KEY: misc feature
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Sequence 3, Application US/10800161
| Publication No. US20040154051A1
| GENERAL INFORMATION:
| APPLICANT: Cade, Rebecca M
| APPLICANT: Lawton, Kay Ann
| TITLE OF INVENTION: INDUCIBLE PROMOTERS
| FILE REFERENCE: A-31089CIP1 |
| CURRENT APPLICATION UNDABER: US/10/800,161 |
| CURRENT FILING DATE: 1999-12-15 |
| PRIOR FILING DATE: 2000-01-11 |
| NUMBER OF SEQ ID NOS: 31 |
| SOFTWARE: Patentin Ver: 2.1 |
| SEG ID NO 3 |
| LENGTH: 1700
                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cade, Rebecca M
APPLICANT: Lawton, Kay Ann
TILE OF INVENTION: INDUCIBLE PROMOTERS
FILE REPERENCE: A-31089CIP1
CURRENT APPLICATION NUMBER: US/10/800,161
CURRENT PILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: 60/171,008
PRIOR PILING DATE: 2000-01-11
PRIOR PILING DATE: 2000-01-11
SOFTWARE: PATENT ON NUMBER: 60/175,519
FINGR PILING DATE: 2000-01-11
SOFTWARE: PATENT ON NUMBER: 60/175,519
FINGR PILING DATE: 2000-01-11
SOFTWARE: PATENT ON NUMBER: 60/175,519
FINGR PILING DATE: 2000-01-11
SOFTWARE: PATENT ON NUMBER: 60/175,519
FINGR PILING DATE: 2000-01-11
SOFTWARE: PATENT ON NUMBER: 2.1
                                                                                RESULT 5
US-10-800-161-24
i Sequence 24, Application US/10800161
i Publication No. US20040154051A1
GENERAL INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.4%;
Best Local Similarity 99.6%;
Matches 273; Conservative (
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US-10-800-161-3
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181 GACGGCTATAAGAGTTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTC 240
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NAME/KEY: misc feature LOCATION: (646\overline{\Gamma}..(665) OTHER INFORMATION: CAMV AS1 salicylic acid response element
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.4%; Score 272.4; DB 7;
99.6%; Pred. No. 4.1e-60;
trive 0; Mismatches 1;
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Sequence 3.4.3
Sequence 3.4.4
Publication No. US20040248303A1
GENERAL INFORMATION:
APPLICANT: Cade, Robecca M
TITLE OF INVENTION: Inducible Promoter Fragment
FILE REFERENCE: A.31089D1V;
CURRENT APPLICATION NUMBER: US/10/760,752
CURRENT FILING DATE: 2004-01-20
FRIOR APPLICATION NUMBER: 09/733685
FRIOR APPLICATION NUMBER: 60/733685
FRIOR APPLICATION NUMBER: 60/733685
FRIOR APPLICATION NUMBER: 60/731685
FRIOR APPLICATION NUMBER: 60/731685
FRIOR APPLICATION NUMBER: 60/711,008
FRIOR APPLICATION NUMBER: 60/175,519
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219 AAAATCAGCAAATAATTTTTTTTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
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19.3%; Score 52.8; DB 7; Length 509;
Best Local Similarity 96.4%; Pred. No. 0.0015;
Matches 54; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-76-752-1
; Sequence 1, Application US/10760752
; Publication No. US20040248303A1
; GENERAL INFORMATION:
; APPLICANT: Cade, Rebecca M
; APPLICANT: Cade, Rebecca M
; TITLE OF INVENTION: Inducible Promoter Fragment
; TILE REFERENCE: A-31089DIV
; CURRENT FILING DATE: 2004-01-20
; PRIOR PILLING DATE: 2000-12-8
; PRIOR PILLING DATE: 2000-12-8
; PRIOR PILLING DATE: 2000-12-8
; PRIOR PILLING DATE: 2000-12-8
; PRIOR PILLING DATE: 2000-01-11
; SUGTHARE OF SEC ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEC ID NO
                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: CDS
LOCATION: (68)..(433)
OTHER INFORMATION: gene product NI16
FEATURE:
NAME/KEY: misc_feature
LOCATION: (142)..(147)
OTHER INFORMATION: Sall site
CURRENT FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: 60/171,008
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/175,519
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
LENGTH: 509
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ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (68)..(433)
OTHER INFORMATION: gene product N116
                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Arabidopsis thaliana
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LOCATION: (344)..(349)
CTHER INFORMATION: ECORI site
US-10-760-752-1
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NAME/KEY: misc feature
LOCATION: (344)...(349)
CTHER INFORMATION: ECORI site
US-10-800-161-1
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NAME/KEY: misc_feature
LOCATION: (142)...(147)
OTHER INFORMATION: Sall site
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99.4%; Score 272.4; DB 8; Length 1700;
Best Local Similarity 99.6%; Pred. No. 4.1e-60;
Matches 273; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (646)..(665)
OTHER INFORMATION: CAMV AS1 salicylic acid response element
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NAME/KEY: misc feature

LOCATION: (863)..(1228)

OTHER INFORMATION: NI16 genomic coding region
US-10-760-752-3
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; Sequence 1, Application US/10800161
; Publication No. US20040154051A1
; GENERAL INFORMATION:
    APPLICANT: Cade, Rebecca M
    APPLICANT: Dietrich, Robert A
    APPLICANT: Lawton, Kay Ann
    TITLE OF INVENTION: INDUCIBLE PROMOTERS
    FILE REPERENCE: A-31089GLE1
    CURRENT APPLICATION NUMBER: US/10/800,161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (757)..(762)
OTHER INFORMATION: HEXAMERAT 4 element
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (609)..(614)
OTHER INFORMATION: MYCATR22 element
                                                                                                                                   TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (426)..(435)
OTHER INFORMATION: TCA1 motif
                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (365)..(374)
OTHER INFORMATION: TCA1 motif
       PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: Misc feature LOCATION: (707)..(712) OTHER INFORMATION: PAL BOX
                                                                                                           LENGTH: 1700
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US-10-800-161-1
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US-10-027-632-112106
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ORGANISM: Human
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LENGTH: 2469
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                                                                                                                                                                                           RESULT 10
US-10-027-632-102510/c

j Sequence 102510, Application US/10027632

j Publication No. US20020198371A1

j GENERAL INFORMATION:

j APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: IDentification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108027.129

CURRENT PILING DATE: 2002-04-30

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-00-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

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PRIOR FILING DATE: 1999-08-09

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PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09
                                                      219 AAAATCAGCAAATAATTTTTTTTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                AAAATCAGCAAATAAACTTTTCTTGACTAAGCTTAAACGACGCCGTTAACATTTTC
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Pred. No. 0.74;
0; Mismatches 106; Indels
2; Indels
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      Mismatches
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50.2%;
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      54; Conservative
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Best Local Similarity
Matches 107; Conserv
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US-10-027-632-102510
         Matches
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2169 AAAATTATCTGAAATATACTTTCCTTATTGAGAATTTCACAAAATTAAGATCTCAAAAC 2110
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US-10-027-632-102511/c

Sequence 10251, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Delymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108927.129

CURRENT APPLICATION NUMBER: US/10/027, 632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR PLING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1000-02-24

PRIOR FILING DATE: 1000-02-24

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

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Publication No. US20330204075A9

GREEAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION:

POLYMORPHICAN: POLYMORPHISMS in the Human Genome

TITLE OF INVENTION:

POLYMORPHICANION POLYMORPHISMS in the Human Genome

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT PILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

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PRIOR FILING DATE: 2000-07-20
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Matches 107; Conservative C
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US-10-027-632-112106
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ORGANISM: Human
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PELING DATE: 2002-04-30
FRIOR PILING DATE: 2000-07-12
FRIOR PAPLICATION NUMBER: US 60/198,676
FRIOR PILING DATE: 2000-04-20
FRIOR PILING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-24
FRIOR PELING DATE: 2000-03-29
FRIOR PILING DATE: 2000-02-4
FRIOR PELING DATE: 2000-02-4
FRIOR PELING DATE: 1999-11-23
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FRIOR FILING DATE: 1999-09-08
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Pred. No. 0.74;
0; Mismatches 106; Indels 0
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50.2%;
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50.2%;
                                                                                                                     Best Local Similarity 50.28 Matches 107; Conservative
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Best Local Similarity
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; ORGANISM: Human
US-10-027-632-102510
           US-10-027-632-112106
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15.8%; Score 43.4; DB 6; Length 2469;
Best Local Similarity 50.2%; Pred. No. 0.74;
Matches 107; Conservative 0; Mismatches 106; Indels 0
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-28
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Sequence 39222, A
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Sequence 59119, A
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2599, Ap
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                        GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
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US-11-124-368A-2918
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Maximum Match 100%
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2, Appli
36299, A
36299, A
29212, A
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64, Appl
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APPLICANT: POULGEN, KIRSTEN V.

APPLICANT: NIELSEN, KIRSTEN V.

TITLE REFERENCE: 09138 6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT APPLICATION NUMBER: 60/567,570

PRIOR PRILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107
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Pred. No. 1.2;
0; Mismatches 85; Indels 0
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US-10-750-623-31590
US-10-750-185-56349
US-10-240-708-17
US-11-121-086-64
US-11-121-086-104
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US-10-750-623-37833
US-10-793-626-4227
US-10-392-234A-66
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Publication No. US20050260667A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Chumakov, Ilya
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Best Local Similarity 51.4
Matches 90; Conservative
                                                          ) ORGANISM: Homo sapiens
US-11-121-086-107
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NAME/KEY: exon
LOCATION: 237406..237428
OTHER INFORMATION: exon Nbis complement g34872 gene
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CCOATION: 215819..215975
OTHER INFORMATION: exon Rbis complement g34872 gene
FRATURE:
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LOCATION: 216661..216952
JTHER INFORMATION: exon Qbis complement g34872 gene
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LOCATION: 231272..231412
OTHER INFORMATION: exon Obis complement g34872 gene
  OTHER INFORMATION: 3'regulatory region g35018 gene
FEATURE:
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NAME/KEY: misc_feature
LOCATION: 213818..215818
OTHER INFORMATION: 3'regulatory region g34872 gene
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LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene
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NAME/KEY: exon
LOCATION: 231870..231879
OTHER INFORMATION: exon O1 complement g34872 gene
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NAME/KEY: exon
LOCATION: 217027..217061
OTHER INFORMATION: exon Q1 complement g34872 gene
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LOCATION: 229647..229742
OTHER INFORMATION: exon X complement g34872 gene
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LOCATION: 215819..215941
OTHER INFORMATION: exon R complement g34872 gene
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NAME/KEY: exon
LOCATION: 216661..217061
OTHER INFORMATION: exon Q complement g34872 gene
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LOCATION: 230408..230721
OTHER INFORMATION: exon P complement g34872 gene
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OTHER INFORMATION: exon O complement g34872
FEATURE:
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NAME/KEY: exon
LOCATION: 201188..201234
OTHER INFORMATION: exon S g35030 gene
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LOCATION: 214676..214793
OTHER INFORMATION: exon T 935030 gene
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LOCATION: 215702..215746
OTHER INFORMATION: exon U g35030 gene
FRATURE:
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LOCATION: 216836..216915
OTHER INFORMATION: exon V g35030 gene
                                                                  NAME/KEY: exon
LOCATION: 94124..94964
OTHER INFORMATION: exon g35017
APPLICANT: Bougueleret, Lydie
APPLICANT: Balain, Bernard
APPLICANT: Balain, Bernard
APPLICANT: Balain, Bernard
APPLICANT: Balain, Bernard
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
TILE REPERBNCE: 53.0516.DIV
CURRENT APPLICATION NUMBER: US/10/147,603
PRIOR APPLICATION NUMBER: US/10/147,603
PRIOR APPLICATION NUMBER: US/10/147,603
PRIOR APPLICATION NUMBER: US/10/126,903
PRIOR PLING DATE: 1999-03-30
PRIOR PLING DATE: 1999-04-30
PRIOR PLING DATE: 1999-04-30
PRIOR PLING DATE: 1999-04-30
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NAME/KEY: misc feature
LOCATION: 31..1107
COTHER INFORMATION: 5'regulatory region g35018 gene
FEATURE:
NAME/KEY: exon
LOCATION: 1108..1289
FEATURE:
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LOCATION: 18778..18862
OTHER INFORMATION: exon Bbis g35018 gene
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LOCATION: 65505..65853
OTHER INFORMATION: exon G g35018 gene
FEATURE:
NAME/KEY: misc_feature
LOCATION: 65854..67854
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LOCATION: 14877..14920
OTHER INFORMATION: exon B 935018 gene
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LOCATION: 29388..29502
OTHER INFORMATION: exon D 935018 gene
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NAME/KEY: exon
LOCATION: 29967..30282
OTHER INFORMATION: exon E g35018 gene
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LOCATION: 64666..64812
OTHER INFORMATION: exon F 935018 gene
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ORGANISM: Homo sapiens
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LENGTH: 319608
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NAME/KEY:
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345257 Arriggreiraacaarriecraaacrirriargarecraricaarcraaaccgreaara 345198
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TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 ATTIAGTIGITGACAATATCGACCGTCTAAGTTCCACACCGACGGCTATAAGAGTTTCAT
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US-10-750-185-59119

Sequence 59119, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION:
APPLICANT: WAI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: RANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: MAINIOG-2
CURRENT PILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN Version 3.1
SEQ ID NO 59119

LENGTH: 1765
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Pred. No. 1e+02;
0; Mismatches 79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
11.9%; Score 32.6; DE
Best Local Similarity 50.3%; Pred. No. 1e+05
Matches 80; Conservative 0; Mismatches
                                       FILE REFERENCE: ARCD:309US
CURRENT APPLICATION WUMBER: US/11/117,187
CURRENT APPLICATION WUMBER: US/09/531,120
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.1
SOFTWARE: 1082144
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; ORGANISM: Bovine 19866880452391
US-10-750-185-59119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CRGANISM: Arabidopsis thaliana
US-11-117-187-211
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Best Local Similarity
Matches 59; Conserva
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Pred. No. 2.9;
0; Mismatches 72; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 240528..240596
OTHER INFORMATION: exon M1090 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 240528..240617
OTHER INFORMATION: exon M1069 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
COCATION: 240528..240824
JTHER INFORMATION: exon M862 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 240800..240993
OTHER INFORMATION: exon MS1 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRATURE:
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LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene
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OTHER INFORMATION: exon MS2 complement g34872 gene
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OTHER INFORMATION: exon M1 complement g34872 gene
                                                                                                                                       WIHER INFORMATION: exon N2 complement g34872 gene
                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 239719..239853
OTHER INFORMATION: exon N complement g34872 gene
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                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 240528..240569
OTHER INFORMATION: exon M1117 complement g34872
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LOCATION: 240528..240994
DIHER INFORMATION: exon M692 complement g34872
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Best Local Similarity 52.77,
Best Local Similarity 52.77,
These 81, Conservative
                                                                                                       239719..239807
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LOCATION:
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RESULT

Sequence 211, Application US/11117187; Publication No. US20050266560A1; GENERAL INFORMATION: APPLICANT: PREUSS, DAPHNE APPLICANT: COPENHAVER, GREGORY

RESULT 3 US-11-117-187-211/c

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TYPE: DNA ORGANISM: Rattus norvegicus
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Matches 43; Conservative
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US-10-240-708-73/c
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Publication No. US20050287559A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: James J. Devlin

APPLICANT: James J. Devlin

APPLICANT: May Luke

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

TITLE OF INVENTION NUMBER: US/11/124,368A

CURRENT FILING DATE: 2006-05-09

PRIOR FILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-11-09

NUMBER OF SEQ ID NOS: 21112

SEQ ID NO 2918

LEAGTH: 100000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         936 adrigaaaacrcrgrccacacagaaarcrgcacacagaggrriacaggagriragrcara 995
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Sequence 59119, Application US/10750623

Publication No. US20050287531A1

GENERAL INFORMATION:
APPLICANT: MMIGROUNCS, INC.
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: FANTIN, Dennis
TILLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILIOG-1
CURRENT PLING DATE: 2003-12-31
FILE OF INVENTION NUMBER: US/10/750,623
FILE REPERENCE: MMILIOG-1
CURRENT APPLICATION NUMBER: US/10/750,623
FILE REPERENCE: MMILIOG-1
CURRENT PALLOGATE: 2002-12-31
FRIOR PLING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE PATENTING DATE: 2002-12-31
SEQ ID NOS: 64922
SOFTWARE PATENTING DATE: 2005-12-31
SEQ ID NOS: 64922
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SEQ ID NOS: 64922
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SEQ ID NOS: 64922
SERVINGE: PATENTING DATE: 2005-12-31
SEQ ID NOS: 64922
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57555,
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57546,
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57562,
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57545,
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57561,
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LOCATION: 57531, 57532, 57533, 57534,
LOCATION: 57540, 57541, 57542, 57543,
LOCATION: 57540, 57540, 57550, 57551,
LOCATION: 57556, 57557, 57558, 57559,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bovine 19866880452391
US-10-750-623-59119
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57573, 57574, 5
57581, 57582, 5
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LOCATION: 57564, 57565,
LOCATION: 57573, 57574,
LOCATION: 57581, 57582,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 59; Conserv
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; TYPE: DNA
; ORGANISM: Bovine 19866881347877
US-10-750-623-39222
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                                                                        253 AAACGAC 259
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SEQ ID NO 37551
LENGTH: 1272
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; Publication No. US20050260603A1
; GENERAL INFORMATION:
APPLICANT: MI GENOMICS, INC.
APPLICANT: MERNORISE, Sue K.
APPLICANT: APPLICANT: RERR Richard
APPLICANT: RERRS Richard
APPLICANT: ROSENFELD, David
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TITLE REPRESENCE: MAIL100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN Version 3.1
SENOTH. 1110.
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                        11.4%; Score 31.2; DB 6; Length 5
45.8%; Pred. No. 46;
tive 0; Mismatches 128; Indels
       PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
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ORGANISM: Bovine 19866881347877
                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 108; Conservative
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US-10-750-185-39222
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| Sequence 39222, Application US/10750623
| Sequence 39222, Application US/10750623
| Publication No. US20050287531A1
| GENERAL INFORMATION:
| APPLICANT: PMISE, Sue K.
| APPLICANT: ROSENFELD, David
| APPLICANT: ROSENFELD, David
| APPLICANT: PANTIN, Dennis
| APPLICANT: PANTIN, Dennis
| APPLICANT: PANTIN, Dennis
| TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
| FILE REPERENCE: MM1110-1
| CURRENT APPLICATION NUMBER: US/10/750,623
| FILE REPERENCE: MM110-1
| CURRENT PAPLICATION NUMBER: US/312-31
| PRIOR FILING DATE: 2003-12-31
| PRIOR FILING DATE: 2003-12-31
| SEQ ID NOS: 64922
| SEQ ID NOS: 64922
| SEQ ID NOS 99222
| LENGTH: 1140
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SEQUENCE 37551, Application US/10750185

Publication No. US200260603A1

GENERAL INFORMATION:

APPLICANT: MI GENOMICS, INC.

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: PANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE SEFERENCE: MAILION-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE PARENT VERSION 3.1
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11.3%; Score 31; DB 6; Length 1140;
Best Local Similarity 52.8%; Pred. No. 32;
Matches 67; Conservative 0; Mismatches 60; Indels
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APPLICANT: Wyeth APPLICANT: Burc
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Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyent
APPLICANT: Wounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
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APPLICANT: HOLM, TOM
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-1
CURRENT APPLICATION NUMBER: 2010-131
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 37551
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Pred. No. 33;
                                                                          Length 1272;
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                                                                                                                   Indels
                                                                                                                   75;
                                                                          Score 31; DB 6;
Pred. No. 33;
0; Mismatches 75
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Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: ROSENTELD, David
; TYPE: DNA
; ORGANISM: Bovine 19866880663412
US-10-750-185-37551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Bovine 19866880663412
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milarity 50.3%;
Conservative 0
                                                                          11.3%;
ilarity 50.3%;
Conservative (
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Best Local Similarity
                                                                        Query Match
Best Local Similarity
Matches 76; Conserv
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                          138 TTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGACGGCTATAAGAGTTT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 TITICIGIATITIACTAAAATICATGGTCTTCAAATATACAAAATAAAGTAAGAATGTTCT 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERBNCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/5714,294
PRIOR PILING DATE: 2005-05-26
                                                                                                                                                                                                                                                                                                                                                             Gaps
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APPLICANT: Muchael
APPLICANT: Twine, Natalie
APPLICANT: Twine, Andrew
APPLICANT: Dorner, Andrew
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 CCTAAWWAWWWWWWWAAAARRWWAWAWWWTAGTTTCCTTTTTACT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.3%; Score 31; DB 7; Length 2217; 45.0%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 CATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTCTTGACT
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                                                                                                                                                                                                                                                                                                        Score 31; DB
Pred. No. 34;
CURRENT APPLICATION NUMBER: US/11/136,527
                     CURRENT FILING DATE: 2005-05-25
PRIOR PAPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SPOFTWARE: PatentIn version 3.2
SEQ ID NO 6695
LENGTH: 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2599, Application US/11136527; Publication No. US20050287570A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 206, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 2599
LENGTH: 2217
                                                                                                                                                                                                                                                                                                        11.3%;
                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Rattus norvegicus US-11-136-527-2599
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Best Local Similarity
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Matches 49; Conserv
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105 ATGNIGICATIAGCATCAATCICCACCGICCAAITTATTAGTIGITGACAAIAICGACC 164
421 IGACTAIGAATATTAICGGAITACTGAATTGIATCAAITTGITTGITTGIATCAAIAICAAGAATATCAGCT 4480
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                                                                                                                                      Gaps
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0
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Best Local Similarity 47.2%; Pred. No. 64;
Matches 93; Conservative 0; Mismatches 104; Indels 0.
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; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 206
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-206
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Search completed: January 12, 2006, 02:38:32 Job time : 401 secs

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us-10-800-161-28.rni

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US-09-733-685-3; Application US/09733685; Patent No. 6706952
                                                                                                                                                           January 12, 2006, 00:16:10 ; Search time 148 Seconds (without alignments) 3290.891 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                              1 tctagaaatatagccgatac......acgacgccgttaacattttc 274
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2: /cgm2 6/ptodata/1/ina/5_COMB.seq:*
3: /cgm2 6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgm2 6/ptodata/1/ina/H_COMB.seq:*
6: /cgm2 6/ptodata/1/ina/PP_COMB.seq:*
7: /cgm2 6/ptodata/1/ina/PP_COMB.seq:*
8: /cgm2 6/ptodata/1/ina/PP_COMB.seq:*
9: /cgm2 6/ptodata/1/ina/RP_COMB.seq:*
9: /cgm2 6/ptodata/1/ina/RP_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
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                                                                                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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		op.			SUMMARIES	
Result No.	Score	Query	Query Match Length DB	DB	ID	Description
1	272.4	4.66	1700	3	US-09-733-685-3	Sequence 3, Appli
2	52.8	19.3	509	m	US-09-733-685-1	Sequence 1, Appli
o O	39	14.2	601	ო	US-09-949-016-83537	Sequence 83537, A
4	39	14.2	49440	m	US-09-949-016-14150	Sequence 14150, A
Ω.	37.8	13.8	319608	٣	US-09-539-333D-1	Sequence 1, Appli
ø	37.8	13.8	319608	m	US-09-679-409-1	Ä
7	37.2	13.6	1852	'n	US-09-813-356-2	'n
8	37.2	13.6	1963	٣	US-09-813-356-1	Sequence 1, Appli
6	37.2	13.6	1963	٣	US-09-813-356-3	Sequence 3, Appli
c 10	35.4	12.9	30002	٣	US-09-949-016-15866	Sequence 15866, A
c 11	34.6	12.6	1141	ო	US-09-806-708B-22	
c 12	34.4	12.6	227390	m	US-09-949-016-12201	
c 13	34.4	12.6	227391	m	US-09-949-016-13365	٠.
c 14	34.2	12.5	601	m	US-09-949-016-112718	Seguence 112718,
c 15	34.2	12.5	601	٣	US-09-949-016-112802	Sequence 112802,
c 16	34.2	12.5	601	m	US-09-949-016-112886	Seguence 112886,
Н	34.2	12.5	601	e	US-09-949-016-112962	Sequence 112962,
c 18	34.2	12.5	601	ᠻ	US-09-949-016-113048	Sequence 113048,
-	34.2	12.5	127280	m	US-09-949-016-14857	Sequence 14857, A
7	34.2	12.5	132266	m	US-09-949-016-14860	
~	34.2	12.5	150833	m	US-09-949-016-14859	
c 22	34.2	12.5	159963	ņ	US-09-949-016-14858	14858,
c 23	34.2	12.5	171130	m	US-09-949-016-14861	Sequence 14861, A
24	34	12.4	2275	7	US-08-743-637B-2	Sequence 2, Appli

Sequence 2, Appli	Sequence 18033, A	Sequence 2708, Ap	Sequence 46, Appl	Sequence 263, App	Sequence 15274, A	Sequence 2813, Ap	Sequence 17535, A	Sequence 13703, A	Sequence 29, Appl	Sequence 29, Appl	Sequence 1274, Ap	Sequence 36, Appl	Sequence 17030, A	Sequence 11782, A	Sequence 13280, A	Sequence 13994, A	Sequence 11778, A	Sequence 19031, A	Sequence 15009, A	Sequence 1, Appli
US-08-526-840B-2	US-09-621-976-18033	US-09-949-016-2708	US-09-220-132-46	US-09-949-016-263	US-09-949-016-15274	US-09-621-976-2813	US-09-949-016-17535	US-09-949-016-13703	US-08-743-637B-29	US-08-526-840B-29	US-09-540-236-1274	US-09-596-002-36	US-09-949-016-17030	US-09-949-016-11782	US-09-949-016-13280	US-09-621-976-13994	US-09-949-016-11778	US-09-513-999C-19031	US-09-270-767-15009	US-08-916-421B-1
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2.4	2.3	2.3	2.3	2.3	2.3	12.2	12.2	12.2	12.1	12.1	12.1	12.1	12.1	12.1	12.1	12.0	12.0	12.0	12.0	12.0
ä	H	H	H	Ä	H	H	H	H	H	H	H	H	H	-	H	H	H	H	H	H
34	33.6	33.6	33.6	33.6	33.6	33.4	33.4	33.4	33.2	33.2	33.2	33.2	33.2	33.2	33.2	33	33	32.8	32.8	32.8
25	26	27	28	5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

JAPPLICANT: Cade, Rebecca M
APPLICANT: Cade, Rebecca M
APPLICANT: Dietrich, Robert A
TITLE OF INVENTION: GERES ENCODING PROTEINS INVOLVED IN THE REGULATION OF
TITLE OF INVENTION: SAR GENE EXPRESSION IN PLANTS
TITLE OF INVENTION: SAR GENE EXPRESSION IN PLANTS
FILE REPERENCE: A-31089A
CURRENT APPLICATION NUMBER: U5/09/733,685
CURRENT APPLICATION NUMBER: 60/171,008
PRIOR PRILING DATE: 1999-12-15
PRIOR PLILING DATE: 1999-12-15
PRIOR PLILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 23
SCHUARER PALENTIN VET: 2.1
SEQ ID NO 3
LENGTH: 1700 NAME/KEY: misc feature
LOCATION: (609)..(614)
OTHER INFORMATION: WACATR22 element
NAME/KEY: misc feature
LOCATION: (646)..(665)
OTHER INFORMATION: CAMV ASI salicylic acid response element
NAME/KEY: misc feature
LOCATION: (700)..(712)
OTHER INFORMATION: PAL BOX NAME/KEY: misc feature
LOCATION: (757)..(762)
OTHER INFORMATION: HEXAMERAT 4 element
NAME/KEY: misc feature
LOCATION: (863)..(1228)
OTHER INFORMATION: NI16 genomic coding region
US-09-733-685-3 TYPE: DNA
ORCANISM: Arabidopsis thaliana
FRATURE:
NAME/KEY: misc feature
LOCATION: (365)...(374)
OTHER INFORMATION: TCA1 motif
NAME/KEY: misc feature
LOCATION: (426)...(435)
OTHER INFORMATION: TCA1 motif GENERAL INFORMATION:

Query Match

99.4%; Score 272.4; DB 3; Length 1700;

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Fatent No. 676852

GENERAL INFORMATION:
APPLICANT: Cade, Rebecca M

APPLICANT: Cade, Rebecca M

TITLE OF INVENTION: GENES ENCODING PROTEINS INVOLVED IN THE REGULATION OF

TITLE OF INVENTION: SAR GENE EXPRESSION IN PLANTS

CURRENT PILING DATE: 2000-12-08

CURRENT FILING DATE: 1999-12-15

FRIOR APPLICATION NUMBER: 60/175,519

FRIOR APPLICATION NUMBER: 60/175,519

FRIOR APPLICATION NUMBER: 60/175,519

FRIOR APPLICATION NUMBER: 60/175,519

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                                                                                                                                                                                                                                                                        757
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                                                                                         578 TCTAAAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTTTCCAAAGTCA
                                                                                                                                                                       CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACAC
                                                                                                                                                                                                                                                                                                                GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTC
                                                          1 TCTAGAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                     Gaps
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                     1; Indels
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Pred. No. 1.2e-05;
0; Mismatches 2;
  Pred. No. 5.8e-68;
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                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS

CCATION: (68)..(433)

THER INFORMATION: gene product NI16

NAME/KEY: misc feature

CCATION: (1427)..(147)

OTHER INFORMATION: Sall site

NAME/KEY: misc feature

CATION: (3447)..(349)

US-09-733-685-1
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; Sequence 83537, Application US/09949016
; GENERAL NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 AAAATCAGCAAATAATTTTT
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 96.4%;
Matches 54; Conservative
99.68;
  Best Local Similarity 99.6
Matches 273; Conservative
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US-09-949-016-14150

Sequence 14150, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSECSEQ for Windows Version 4.0

SEQ ID NO 14150

LENGTH: 49440
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT ELLOS CLOOL304
CURRENT APPLICATION NUMBER: 06/241,755
RICOR APPLICATION NUMBER: 06/241,755
RICOR APPLICATION NUMBER: 06/241,756
RICOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PELLING DATE: 2000-10-03
PRIOR PELLING DATE: 2000-10-03
PRIOR PELLING DATE: 2000-09-06
RICOR APPLICATION NUMBER: 60/231,498
REOR PELLOR PRIOR NUMBER: 06/231,498
REOR FILING DATE: 2000-09-06
REOR APPLICATION NUMBER: 06/231,498
REOR FILING DATE: 2000-09-06
REOR APPLICATION NUMBER: 60/231,498
REOR FILING DATE: 2000-09-06
REOR APPLICATION NUMBER: 60/231,498
REOR FILING DATE: 2000-09-06
REOR APPLICATION NUMBER: 60/231,498
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REOR FILING DATE: 2000-09-09-06
REOR APPLICATION NUMBER: 60/231,498
REOR FILING DATE: 2000-09-09-09
REOR APPLICATION NUMBER: 60/231,498
REOR FILING DATE: 2000-09-09-09
REOR APPLICATION NUMBER: 60/231,498
REOR FILING DATE: 2000-09-09-09
REOR FILING DATE: 2000-09-09-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 TGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCATCAATCTCC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                576 TGTATTCATGACAGTTTCTATATATATTGAACATTAGGGTCACATGATATATTTTTTT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 ACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGACGGCTA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          516 ggccrcrcacarrrgrcacrrarcagraricarcrrrccaarcagcacacacacrr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.2%; Score 39; DB 3; Length 601; 51.4%; Pred. No. 0.11; ive 0; Mismatches 85; Indels
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Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.4
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-949-016-83537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human
US-09-949-016-14150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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COCATION: 215819..215975
THER INFORMATION: exon Rbis complement g34872 gene
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LOCATION: 216661..216952
JTHER INFORMATION: exon Qbis complement 934872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 231272..231412
OTHER INFORMATION: exon Obis complement g34872 gene
                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: 65854..67854
OTHER INFORMATION: 3'regulatory region g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: 213818..215818
OTHER INFORMATION: 3'regulatory region g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 217027..217061
OTHER INFORMATION: exon Q1 complement 934872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene
FRAVURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 215819..215941
OTHER INFORMATION: exon R complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAWE/KEY: exon
LOCATION: 229647..229742
OTHER INFORMATION: exon X complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: exon
LOCATION: 216661..217061
OTHER INFORMATION: exon O complement g34872 gene
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OTHER INFORMATION: exon P complement 934872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 214676..214793
COTHER INFORMATION: exon T g35030 gene
FRATURE:
NAME/KEY: exon
LOCATION: 215702..215746
OTHER INFORMATION: exon U g35030 gene
FRATURE:
NAME/KEY: exon
LOCATION: 216836..216915
OTHER INFORMATION: exon V g35030 gene
OTHER INFORMATION: exon V g35030 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAMEN Excess
LOCATION: 201188..201234
OTHER INFORMATION: exon S g35030 gene
                                               OTHER INFORMATION: exon F 935018 gene
                                                                                                                                                                    G g35018 gene
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 94124..94964
OTHER INFORMATION: exon g35017
                                                                                                        NAME/KEY: exon
LOCATION: 65505..65853
OTHER INFORMATION: exon
                      64666..64812
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NAME/KEY:
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Chen, Daniel
APPLICANT: Chen, Daniel
APPLICANT: Chen, Daniel
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenfeld, Marta
APPLICANT: Bouguelerer, Lydie
APPLICANT: Bouguelerer, Lydie
APPLICANT: Bouguelerer, Lydie
APPLICANT: Bailani, Bernard
APPLICANT: Bailani, Bernard
APPLICANT: Besioux, Laurent
TITER OF INVERTION: SCHIZOPHERNIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
FILE REPERENCE: GENSET 047AUS
CURRENT APPLICATION NUMBER: US 60/136, 903
PRIOR APPLICATION NUMBER: US 60/132, 065
PRIOR APPLICATION NUMBER: US 60/132, 065
PRIOR PELING DATE: 1999-04-30
PRIOR PELING DATE: 1999-07-19
PRIOR PELING DATE: 1999-07-29
PRIOR PELING DATE: 1999-07-29
PRIOR PELING DATE: 1999-07-29
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PRIOR PELING DATE: 1999-10-12
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PRIOR PELING DATE: 1999-10-12
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                                                     24627 raacarcarrerraaragareraceraarrearrraaraagreerrrerre 24681
NAME/KEY: misc_feature
LOCATION: 31..1107
OTHER INFORMATION: 5'regulatory region g35018 gene
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OTHER INFORMATION: exon Bbis g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: excn
LOCATION: 29388..29502
OTHER INFORMATION: excn D g35018 gene
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NAME/KEY: exon
LOCATION: 29967..30282
OTHER INFORMATION: exon E 935018 gene
FEATURE:
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NAME/KEX: exon
LOCATION: 25593..25740
OTHER INFORMATION: exon C g35018 gene
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LOCATION: 1108..1289
OTHER INFORMATION: exon A 935018 gene
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OTHER INFORMATION: exon B g35018 gene
                                                                                                                                                                                                 Sequence 1, Application US/09539333D Patent No. 6476208
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEATURE:
NAME/KEY: exon
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NAME/KEY: exon
                                                                                                                                                    RESULT 5
US-09-539-333D-1
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VS-003-679-409-1

Sequence 1, Application US/09679409

Sequence 1, Application US/09679409

Sequence 1, Application US/09679409

PAPELICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Bougueleret, Lydie

APPLICANT: Bssioux, Laurent

APPLICANT: Bssioux, Laurent

TILLE OF INVENTION: SCHIZOPHENIA ASSOCIATED GENE, PROTEINS AND BIALLELIC MARKERS

FILE REFERENCE: 5.001-0.03

PRIOR FILING DATE: 2000-03-03

PRIOR FILING DATE: 1099-10-12

PRIOR FILING DATE: 1999-10-12

PRIOR FILING DATE: 1999-10-12

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-11-30

NUMBER OF SEQ ID NOS: 134

SEQ ID NO 1

LENGTH: 319608

TWOR: NANA
                                                                      57915 AAAGGGAGAAAAATGAGGCACCACCTCTTTA 57947
                         158 ATCGACCGTCTAAGTTCCACACCGACGGCTATA 190
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
FRATURE:
NAMEXTEX:
NAMEXTEX:
OTHER INFORMATION: 5'regulatory region
LOCATION: 201123.201234
OTHER INFORMATION: exon S
NAMEX FEX: exon
LOCATION: 201123.201560
OTHER INFORMATION: exon S
OTHER INFORMATION: exon S
OTHER INFORMATION: exon S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 214676..214793
OTHER INFORMATION: exon T
NAME/KEY: exon
LOCATION: 215702..215746
OTHER INFORMATION: exon U
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OTHER INFORMATION: exon V2
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 240440..241153
OTHER INFORMATION: exon W2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 227655..227736
OTHER INFORMATION: exon V4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 238715..238919
OTHER INFORMATION: exon V3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 216836..216994
OTHER INFORMATION: exon V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 217671..217764
OTHER INFORMATION: exon V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 241072..241291
OTHER INFORMATION: exon X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 240440..240673
OTHER INFORMATION: exon W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 TCGCATGATGATGTCATTAGCATCAATCTCCACCGTCCAATTTATTAGTTGTTGACAAT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 GACTICCITIATICCAAAAGICAAIAAAGIGIGACGICAIGAIACITAACGCITIAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
13.8%; Score 37.8; DB 3; Length 319608;
Best Local Similarity 52.9%; Pred. No. 1.1;
Matches 81; Conservative 0; Mismatches 72; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon
JOCATION: 240528..240569
OTHER INFORMATION: exon M1117 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANME/KEY: exon
LOCATION: 240528..240596
OTHER INFORMATION: exon M1090 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEY: exon
ION: 240528..240617
INFORMATION: exon M1069 complement g34872 gene
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LOCATION: 240528..240994
OTHER INFORMATION: exon M692 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
COCATION: 240528..240824
OTHER INFORMATION: exon M862 complement g34872 gene
                                                                                                                                                                      NAME/KEY: exon
COGATION: 237406..237428
OTHER INFORMATION: exon Nbis complement g34872 gene
FEATURE:
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NAME/KEY: misc_feature
LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene
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NORME/KEY: exon
NOCATION: 240528..240644
OTHER INFORMATION: exon MS2 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 240800..240993
OTHER INFORMATION: exon MS1 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory region g34872 gene
                                                                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 239719..239807
OTHER INFORMATION: exon N2 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 240528..241685
JTHER INFORMATION: exon M1 complement g34872 gene
LOCATION: 231870..231879
OTHER INFORMATION: exon O1 complement g34872 gene
                                                                    NAME/KEY: exon
LOCATION: 234174..234321
OTHER INFORMATION: exon 0 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: exon
LOCATION: 239719..239853
THEN INFORMATION: exon N complement g34872 gene
FEATURE:
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LOCATION: 292653..292841
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: variable motif AAAGG or GAAGGAAGGAAGGAAGA
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Pred. No. 1.1;
0; Mismatches 72; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: 210361
OTHER INFORMATION: 8-283-278 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 210463
OTHER INFORMATION: 8-283-176 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 210466
OTHER INFORMATION: 8-283-153 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 210583
OTHER INFORMATION: 8-283-56 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 21087
OTHER INFORMATION: 8-282-345 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 210964
OTHER INFORMATION: 8-282-260 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 210979
OTHER INFORMATION: 8-282-245 : polymorphic base A or C
NAME/KEY: allele
LOCATION: 210979
OTHER INFORMATION: 8-282-245 : polymorphic base A or C
NAME/KEY: allele
LOCATION: 211050
OTHER INFORMATION: 8-282-174 : variable motif AAAGG or GAAC
OTHER INFORMATION: 8-282-174 : variable motif base A or T
NAME/KEY: allele
LOCATION: 21132
OTHER INFORMATION: 8-282-92 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 211247
OTHER INFORMATION: 8-281-367 : polymorphic base A or G
OTHER INFORMATION: 211247
OTHER INFORMATION: 211247
OTHER INFORMATION: 211247
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  OTHER INFORMATION: 8-293-130 : polymorphic base A or
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LOCATION: 212520
CTHER INFORMATION: 8-279-197 :
NAME/KEY: allele
LOCATION: 212821
CTHER INFORMATION: 8-278-289 ::
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
LOCATION: 209123
OTHER INFORMATION: 8-287-86 :
NAME/KEY: allele
LOCATION: 209631
OTHER INFORMATION: 8-285-319 :
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Best Local Similarity 52.9%;
Matches 4.9.81; Conservative (
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LOCATION: 211315
OTHER INFORMATION: 8-281-299
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                          NAME/KEY: allele
LOCATION: 206545
OTHER INFORMATION: 8
NAME/KEY: allele
LOCATION: 207313
OTHER INFORMATION: 8
NAME/KEY: allele
LOCATION: 208285
OTHER INFORMATION: 8
NAME/KEY: allele
LOCATION: 208260
OTHER INFORMATION: 8
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LOCATION: 211366
OTHER INFORMATION:
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; Sequence 3, Application US/09813356 ; Patent No. 6730826
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Best Local Similarity 47.8%;
Matches 108; Conservative (
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.6%;
Best Local Similarity 47.8%;
Matches 108; Conservative
                                                                                  TYPE: DNA
ORGANISM: Nicotiana tabacum
FEATURE:
NAME/KEY: exon
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                                                                                                                                                                   | LOCATION (1853) .. (1963) | NAME/KEY: CAAT signal | LOCATION (1669) .. (1672) | NAME/KEY: TATA signal | LOCATION (1775) .. (1778) | NAME/KEY: GC signal | LOCATION (1807) | NAME/KEY: promoter | LOCATION (1907) | LOCATION (1) .. (1852) | US-09-813-356-1
                                            SEQ ID NO 1
LENGTH: 1963
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  57855 TTGCTTGTGAATGTCTTTATCTTCAATGTCAGCCGTCCAAAAGAGTAAAAAGAGAAAAAC 57914
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; Sequence 1, Application US/09813356
; Sequence 1, Application US/09813356
; Patent No. 6730826
; GENERAL INFORMATION:
; APPLICANT: Susheng, Gan
; APPLICANT: Erming, Wang
; APPLICANT: Erming, Wang
; TITLE OF INVENTION: Trichome Specific Regulatory Sequence
; FILE REPERBNCE: 50229-260
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,088
; PRIOR PILING DATE: 2000-03-22
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                                                                                                                                                                                   Sequence 2, Application US/09813356
Patent No. 6730826
GENERAL INFORMATION:
APPLICANT: George, Wagner
APPLICANT: Erming, Wang
APPLICANT: Rui, Wang
APPLICANT: Rui, Wang
TITLE CO INVENTION: Trichome Specific Regulatory Sequence
                                                                                  57915 AAAGGGAGAAAAATGAGGCACCACCCTCTTTA 57947
                                               158 ATCGACCGTCTAAGTTCCACACCGACGGCTATA 190
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,088
PRIOR FILING DATE: 2000-03-22
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
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COCATION: (1669)..(1672)

NAME/KEY: GC_Signal

LOCATION: (1806)..(1807)

US-09-813-356-2
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                                                                                                                                                                                                                                                                                                                                                       136 AATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGACGGCTATAAGAGT 195
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                                                                                                              16 GATACCAATTTTTCCACACACGACTTCCTTTATTCCAAAAGTCAATAAAGTGTGACGTC
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Length 1963;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INCORMATION:

APPLICANT: George, Wagner

APPLICANT: Susheng, Gan

APPLICANT: Stateng, Wang

APPLICANT: Erming, Wang

APPLICANT: Rui, Wang

TITLE OF INVENTION: Trichome Specific Regulatory Sequence

FILE REFERENCE: 50229-260

CURRENT APPLICATION NUMBER: US/09/813,356

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/191,088

PRIOR APPLICATION NUMBER: US 60/191,088

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.0

SEQ ID NO 3
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                                                          0, Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 TTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTCT
   DB 3;
Score 37.2;
Pred. No. 0.
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0; Gaps

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; LOCATION: (1)..(1141); OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters US-09-806-708B-22
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                                                                                                                                                                                                                                               566 WYWSINNAMWYRRYSARNWSSMARWTTRINNWWNSGBVRMRWAGTWWWRHWINNNTDTRYYW 507
                                                                                                                                                              46 TIATICCAAAAGICAATAAAGIGIGACGICAIGAIACITAACGCITTAAAAACAICGCAIGA 105
                                                                                                                                                                                                        686 INNTIVMRRRWMINTKTRWYSTTRRHHYTGATNNNNNNNNNNNNNNNNNSCCTCTRMMTMR 627
                                                                                                                                                                                                                                                                                                                                                                                                                                               506 WWKRWARBTTTYYDSMCNAKSMWRGINWRAMKMWWAANNDAGAMDHWTY 458
                                                                                                                                                                                                                                                                                                                                                                                                                    226 GCAAATAATTTTTTTTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                          Query Match
12.6%; Score 34.6; DB 3; Length 1141;
Best Local Similarity 11.4%; Pred. No. 2.2;
Matches 26; Conservative 97; Mismatches 106; Indels 0
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US-09-949-016-13365/c
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US-09-949-016-15866/c
; Sequence 15866, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VEYTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT PILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15866
; LENGTH AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10562 AACTCTCCTCTGGCTTAGTTAGCTTCACACTATATTCCTTGTCTGAATTCCTCGACTT 10503
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    790 TTAGATAATAGTTACTACTATTTGTCATGAAATATCAATAGATACAAATTTAAAGTGAC 849
                                              AATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGACGGCTATAAGAGT 195
                                                                                   850 TATAAATTTACGAGTTTACTATACTTTAGTCGTACAGTTTGCAATAATAGTATTTTAACC 909
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Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR PILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
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                                                                                                                               196 TTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTCT
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ORGANISM: Artificial sequence
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12.9%;
Best Local Similarity 54.1%;
Matches 72; Conservative
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US-09-949-016-15866
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Sequence 12201. Application US/09949016

Sequence 12201. Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SOFTWARE: FRESESE for Windows Version 4.0

SEQ ID NO 12201

LENGTH: 227390
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OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 52.09
Matches 77; Conservative
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72 CGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCATCAATCTCCACC 131
                                                              210 AGGCAACCACAGTTTTGCTTTTTTTTTTTTTTTTAAAAGGAATTATAAAATAGGTA 151
12 AGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCAATAAAGTGTGA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 GAATTTCAGAAGTAATTTT 12
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Best Local Similarity 48.2
Matches 96; Conservative
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ORGANISM: Human
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLO01307
CURRENT PELLOCATION NUMBER: US/09/949,016
CURRENT PELLOCATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FastSEQ for Windows Version 4.0
LENGTH: 601
LENGTH: 601
LENGTH: 601
LENGTH: 601
LENGTH: 601
                         GENERAL INCORDATION: Craig et al.
APPLICANT: VENTER.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
FRICE RAPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRESCE FRE
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Pred. No. 2.5;
0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
12.6%; Score 34.4; DB 3;
Best Local Similarity 52.0%; Pred. No. 9.3;
Matches 77; Conservative 0; Mismatches 71;
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US-09-949-016-112718/c
; Sequence 112718, Application US/09949016
; Patent No. 6812339
Sequence 13365, Application US/09949016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // LOCATION: (1)...(227391)
// OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13365
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Best Local Similarity 48.2%;
Matches 96; Conservative
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LOCATION: (1)...(22739:
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US-09-949-016-112718
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Sequence 112802, Application US/09949016

Sequence 112802, Application US/09949016

Patent No. 681233

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMPRHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TURENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-0-03

PRIOR PLILNG DATE: 2000-0-03

SPRIOR FILING DATE: 2000-0-03

SPRIOR FILING DATE: 2000-0-03

SPRIOR FILING DATE: 2000-0-03

SPRIOR FILING DATE: 2000-0-0-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 CGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCATCAATCTCCACC 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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150 GTCTTTTATATGTCTTTTATATGACATAGCATAATGTCAAACTCATCTTTTGACCACACO 91
                                                                                                                                                  90 CTCAAATATGTTATGTCTCCAACCTTCCTTACCTGGTAAGTGGCACTTCTATTCCAGCCA 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.5%; Score 34.2; DB 3; Length 601;
48.2%; Pred. No. 2.5;
iive 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: January 12, 2006, 02:17:53
Job time : 155 secs
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RESULT
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                                                                       January 12, 2006, 00:02:06 ; Search time 3802 Seconds (without alignments) 3371.820 Million cell updates/sec
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                                                                                                                                                   1 tetagaaatatageegatae......aegaegeegttaaeatttte 274
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                 41078325 seqs, 23393541228 residues
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Maximum Match 100%
Listing first 45 summaries
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A1540689
A1873432
A1290306
A1620654
A1261119
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                                                  using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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274
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Match Length DB
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		BQ003373 UI-H-EII-	BQ006479 UI-H-EI1-	CA447735 UI-H-EIO-	AF116653 Homo sapi				BE219714 hv61e10.x	AI797039 we26b06.x	W96222 ze10g07.81	BM144644 TCAAP1D12		AA700613 zi41d04.8	AW051787 wz03c11.x	AI708670 as39b03.x	BE856347 7f93c07.x	BE501745 hw34f10.x	AI284430 qu51b08.x	N46359 yy74g11.81	AA936680 ol79b04.8	AI435057 th82c12.x
BM995524	BQ015514	BO003373	B0006479	CA447735	AF116653	BP423473	A1494002	AI708269	BE219714	AI797039	W96222	BM144644	BM150022	AA700613	AW051787	AI708670	BE856347	BE501745	AI284430	N46359	AA936680	AI435057
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42	42	4	4 .	42	4.2	41.6	41.6	41.6	41.6	41.6	41.4	41.4	41.4	41.4	41.4	41.4	41.4	41.4	40.4	40	39.8	39.8
23	24	2,5	26	27	78	29	30	31	32	33	34		9 (3.7	38	36	40	4	42	4.3	4 4	45

ALIGNMENTS

1 1	
867	
ITION	SALK 082724.45.05.x Arabidopsis thaliana TDNA insertion lines Arabīdopsis thaliana genomic clone SALK 082724.45.05.x, genomic
	survey sequence.
NOIS	
NO	BZ352867.1 GI:24943729
RDS	
闰	Arabidopsis thaliana (thale cress)
ANISM	Arabidopsis thaliana
	Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
	Spermatophyta; Magnollophyta; euglectyledons; cole euglecyledons;
action	rogids; eurosids II; Brassicales; brassicaceae; Arabiuopsis.
HORS	Jones J. M. Leisse, T.J. Barajas, P., Chen, H., Cheuk, R.,
	Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
	Shinn, P., Zimmerman, J. and Ecker, J.R.
TE	A Sequence-Indexed Library of Insertion Mutations in the
	Arabidopsis Genome
TRNAL	Unpublished (2001)
INI	
	Salk Institute Genomic Analysis Laboratory (SIGnAL)
	The Salk Institute for Biological Studies
	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
	Tel: 858 453 4100 x1752
	Fax: 858 558 6379
	nt.
	equence recovered from the left
	TDNA. This sequence lies within 300 bases of the 5' end of
	Class: TDNA tagged.
RES	Location/Qualifiers
source	
	/organism="Arabidopsis thailana"
	/mol_cype="genomic DNA"
	/ecotype="Co1-0"
شو	
	/clone="SALK_082724.45.05.x"
	/clone_lib="Arabidopsis thaliana TDNA insertion lines"
	/note="PCR was periormed on Arabidopsis Lighted Lines
	each of which contains one or more tunk libertion
	elements. The resultant Iragment for each fine was discoult by semisoned to determine the denomic sequence at
	The site of insertion Details of the protocols used can

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Gaps

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Indels

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вны14587
SALK 066674 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_066674, genomic survey sequence.
BH814587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 237)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Adorinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                               61 ccacccicraagriccacaccccacaccciaraacacriricarraraaarriraccaaaara 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AATAAAATCAGCAAATAATTTTTTTTTTGACTAAGCTGAAGCGAGGGCGGTAACATTCTC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="taxon:3702"
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/clone="SALK 066674"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
                                                                            100 GCATGATGATGATTAGCATCAATTTCCACCGTCCAATTTAATTTAGTTGTTGACAATAŢ
                                                                                                                              160 CGACCGTCTAAGTTCCACACCGACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies
TOULO N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752
Fax: 858 558 6379
Best Local Similarity 100.0%; Pred. No. 2.9e-28; Matches 152; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                              121 AAATCAGCAAATAATTTTTTTCTTGACTAAGCT 152
                                                                                                                                                                                                                                                                                   220 AAATCAGCAAATAATTTTTTTTGACTAAGCT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/ecotype="Col-0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: TDNA tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 111; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
BH814587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
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KEYWORDS
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each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                                                                                                                                                                                                      84 TACGCTTTAAAACATCGCATGATGATGTCATTAGCATCAATCTCCACCGTCCAATTTATT 143
                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                       144 TAGTIGITGACAATATCGACCGTCTAAGTTCCACACCGACGGCTATAAGAGTTTCATTAT 203
                                                                                                                                                                                                                                                                                                                                                                                                                            121 TAGTIGITGACAATATCGACCGTCTAAGTICCACACCGACGACGGCTATAAGAGTITCATTAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 152)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Adorinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                     83
                                                                                                                                                                                                                                 9
     found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BZ770600 152 bp DNA linear GSS 13-MAR-2
SALK 143535.56.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_143535.56.00.x, genomic
                                                                                                                                                                                                                                                                                                                      TACGCTTTAAAACATCGCATGATGATGTCATTAGCATCAATCTCCACCGTCCAATTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At3g25882.
                                                                                                                                                                                     TTTTTCCACACACGACTTCCTTTATTCCAAAAGTCAATAAAGTGTGACGTCATGATACT
                                                                                                                                                                                                                                 TTTTTCCNCNCNTGGACTTCCTTTATTCCNAAAGTCNATANAGTGTGACGTCATGATACT
                                                                                                                                   Gaps
                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis Genome
Unpublished (2001)
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
TH: 858 453 4100 x1752
Fax: 858 558 6379
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                                                                                 Length 228
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/mol_type="genomic DNA"
/ecotype="Col-0"
                                                                              Score 222; DB 9;
Pred. No. 4.3e-46;
                                                                                                                                   0; Mismatches
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Location/Qualifiers
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                                                                                 81.0%;
97.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
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BZ019485.1 GI:23579218
                                   Brassica oleracea
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                                                                 B2352865 14-NOV-2002 SALK 082722.32.45.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_082722.32.45.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="txxon:3702"
/db xref="txxon:3702"
/clone="SALK 082722.32.45.x"
/clone="lb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Class: TDNA tagged.
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                                                                                                                                                                                       Arabidopsis thaliana (thale cress)
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Best Local Similarity 92.7%;
Matches 139; Conservative (
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BP863458 RAFL21 Arabidopsis thaliana cDNA clone RAFL21-66-M11 5', mRNA sequence.
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/mol_type="genomic DNA"
/db_xref="taxon:312"
/clone_lib="B.oleracea002"
/note="Vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO100DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
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Brassica oleracea
Wataryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, euroside II, Brassicales, Brassicaceae, Arabidopsis.
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Seki, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K.,
Iida, K., Enju, A., Sakurai, T., Arakawa, T., Carninci, P., Fukuda, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA-ATAA
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8
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                                                                                                                                  1 (bases 1 to 691)
1 Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: oeg72 row: g column: 05
Seg primer: -28RPPOT reverse
Class: shotgun
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High quality sequence stop: 551.
Location/Qualifiers
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organism="Homo sapiens"
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                                                                                                                                                                                      Fax: 81-298-36-9660
Email: maski@rtc.riken.go.jp
An Arabidopsis exten.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998, 2002).This clone is in a
modified pBluescript vector.
Please visit our web site (http://pfgweb.gsc.riken.jp and
http://rargs.gsc.riken.jp) for further details.
Location/Qualifiers
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Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
3712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Fax: 301 838 0208
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
/mol_type="mRNN"
/db_xref="texton:3702"
/clone="RAFL21-66-M11"
/lab_host="DH10B"
/clone="Lib="RAFL21"
/note="Site_1: BanH1; Site_2: Sall; Subtraction Library.
The sequence was obtained From samples subjected to various stress and plant hormones-treated"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Seg primer: M13-21
Class: BAC ends.
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Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Iida,J., Kawai,J., Sasaki,D., Shiraki,T., Hayashizaki,Y. and
                                       Large-Scale Analysis of RIKEN Arabidopsis Full-length cDNAs Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 17.9%; Score 49; DB 3; Length 397; Best Local Similarity 100.0%; Pred. No. 0.056; Matches 49; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score *>,
Pred. No. 0.056;
_____hes 0; Indels
                                                                             Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae; Homo.
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Donaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NGI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 444.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="NCI_CGAP_GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP_GC4 was prepared, and
se circles were made in vitro. Following HAP purification,
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w840e09.xl NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2499688 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 TAATGAAGTAGGAGGCAAGATTATCCATTGAAGGTATTATTATATGCAGCTCATCTTAA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 CCGTCTAAGTTCCACACACACAGCTATAAGAGTTTCATTATAAATTTTTAGCAAAATAAAA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 609)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Itissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                    /sex="Male"
/cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                         66; Indels
                                                                                                                                                                                                                                                                                                                                               Length
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2499688"
/issue_type="pooled germ cell tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                                                                                                                                                                                                                                         16.6%; Score 45.4; DB
56.3%; Pred. No. 0.47;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 TCAGCAAATATTTTTTTTGACTAAGCTTA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 ACTTCAAATATCTTCACATTAAGATGATTA 238
/mol_type="genomic_DNA"
/db_xref="GDB:7038437"
/db_xref="taxon:9606"
/clone="2003E3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI990512
AI990512.1 GI:5837393
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Query Match
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yp93b07.81 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:194965 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
lst strand cDNA was primed with a Pac I - oligo(dT) primer
this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 147592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                    63 GACTATAACAGAAATCATATTAATATAAATTAATAATACTTCAAATATCTTTCACATT 122
                                                                                                                                                                                                                                                    124 TCTCCACCGTCCAATTTATTTAGTTGACAATATCGACCGTCTAAGTTCCACACCGAC 183
                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Figh quality sequence stops: 260

Figh quality sequence stops: 260

Figh quality sequence royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 692

Figh grainer: Promega -21ml.3

Figh quality sequence stop: 260.

Figh quality sequence stop: 260.
                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                               DB 1; Length 609;
                                                                                                                                                                                                       54; Indels
                                                                                                                                                               Score 43.6; Di
Pred. No. 1.4;
0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:194965"
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                                                                                                                                                             Query Match
Best Local Similarity 58.5%;
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      244 ACTAAGCTTA 253
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R88734
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Econed into the Pac I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Week genoscope.ons.ft)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 889
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                                                                                                                                                                                                                                                                                                                                                      179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 agaagactataacagaaatcatatttaatatattaaaattaatattcatadaatatcittca 123
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                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genome survey sequence T7 end of BAC BACNISALS of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

All06628
ALL06628.1 GI:5622852
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                                                                                                                                                                                                                                                                                                                                                      120 TCAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACAC
                                                                                                                                                                                                                                                                                                                                                                                                             4 TNANATICCATIGAAGGIATIATITATITGCAGCICATCTIAAGIGACAAAATICCATAC
                                                                                                                                                                                                                                                                                              Gaps
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AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTT 3'],
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                                                                                                                                                                                                                              Query Match 15.7%; Score 43; DB 8; Length 321; Best Local Similarity 56.7%; Pred. No. 1.9; Matches 76; Conservative 0; Mismatches 58; Indels
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Drosophila melanogaster
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16.9%; Pred. No. 3.3
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/organism="Drosophila mel
/db_xref="texon:7227"
/clone="BACNISA12"
/clone=lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end:17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 CTTGACTAAGCTTA 253
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/MOL type="mRNA"
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/ Alb host="DH108"
/ Alb host="DH108"
/ Alb host="Dryan: pooled; Vector: pr773D-Pac (Pharmacia) with a modified polylinker; Site=1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbH119%, testis NHT, and B-cell
libraries (fetal lung NbH119%, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Pollowing HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified CDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.B. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
                                                                                                                                                       289 bp mRNA linear EST 19-DEC-1999 wf82511.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2362125 3', mRNA Bequence.
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DEFINITION qm02a04.x1 Soares_NhHMPu_S1 Homo sapiens CDNA clone IMAGE:1880622
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini;
Hominidae, Homo.
1 (Dases 1 to 289)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 498 Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 270.
Location/Qualifiers
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     244 ACTAAGCTTA 253
                                                     123 AAGATGATTA 132
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Matches 75; Conserv
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AI873432
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 957 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIS40689 135 bp mRNA linear EST 14-APR-1999 tn72all.xl NCI_CGAP_Lyml2 Homo sapiens cDNA clone IMAGE:2175068 3' similar to contains element THR repetitive element ;, mRNA
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                                                                                                                                950 MAMAMINATAMAMAMAMAMAHAMHAMAMATATAMINATAMAMAMAMAMAMAMAMATAMITAMI 1009
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/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
Sall; Site_2: Not!; Cloned unidirectionally. Primer:
Oligo dT. Areage insert size 1.25 kb. Life Technologies catalog #: 11547-015"
139 TTATTTAGTTGTTGACAATATGGACCGTCTAAGTTCCACACACCGACGGCTATAAGAGTTTC 198
                                                                                                                                                                                           124 TCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACGGAC 183
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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/db_xref="taxon:9606"
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/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 833 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 322.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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Matches 75; Conservative 0; Mismatches 55; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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AI620654.1 GI:4629780
                                                        AI290306.1 GI:3933080
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KEYWORDS
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Demail: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
End Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Nww-bio.llnl.gov/bbrp/image/image.html
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="poorly differentiated adenocarcinoma with signet ring cell features"
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1 (bases 1 to 421)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
1 (bases 1 to 418)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                      Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Emmert Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/bbrp//lange/lange.html
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Seq primer: 40UP from Gibco

High quality sequence stop: 416.
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                           1. .421
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244 ACTAAGCTTA 253 ò g

123 AAGATGATTA 132

Search completed: January 12, 2006, 02:15:10 Job time : 3811 secs

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Adp55764 Human PRO
Abz35897 Human sec
Abz35431 Human gen
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Abz35565 Human gen
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(without alignments)
3666.919 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                                                                       January 11, 2006, 22:55:15; Search
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ADR17259
ADR16822
ADV66204
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ADW17257
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Adf90715 Human hep Abv77883 Hypoxia-i Ach50239 Human leu Ab132053 Human imm Acl35363 Rice etre Aah51601 Human chr	É.	AC137108 Rice stre Ad108128 Human gen Adt55151 Nucleotid Acf91349 Human SIR Aak80413 Human imm Aas98600 Human gen	Aca23093 Prokaryot Continuation (5 of Ach68922 Human gen Ac135887 Rice stre Ad35476 Novel mou Ad895227 Murine th Adv68084 Biologica
ADF90715 ABV77883 ACH50239 ACH32053 ACL35363 AAH51601	AASO9301 ADW26070 ADW26105 ADD22878 ADD22877 ADW26073 ADW2606106	ACL37108 ADL08128 ADT55151 ACF91349 AAK80413	ACA23093 AAX20248 04 ACH68922 ACL35887 ADO35476 ADS95227 ADV68084
10 6 9 11 3	5 14 10 10 14 14 14	11 12 13 13 6	8 2 11 13 13 13
4779 2026 375 6301 2000 319608	319608 1834 1834 1852 1963 1969	2000 182328 87394 478 589 140036	621 110000 516 2000 2208 2208 2208
115.1 114.2 113.9	13.6 13.6 13.6 13.6	13.6 13.1 12.9 12.9	22.38
4 4 4 8 5 6 7 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	37.72 37.72 37.72 37.72 37.72	37.2 35.6 35.6 35.4 35.4	33.7.2 3.5.2 3.5.2 3.5.2 4.4 8.8 8.8 8.8 8.8
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ALIGNMENTS

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NI16; transgenic; herbicide resistance; mouse-ear cress; promoter; ds.
                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid molecule comprising Arabidopsis NI16 promoter, useful in regulating transcription of coding sequence of
                                                                    Arabidopsis thaliana NI16 promoter DNA #5.
                                                                                                                                                                                                                                           SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                                                                                               Cade RM, Dietrich RA, Lawton KA,
         ADR16847 standard; DNA; 274 BP
                                                                                                                                                                                       15-DEC-1999; 99US-0171008P.
11-JAN-2000; 2000US-0175519P.
08-DEC-2000; 2000US-00733685.
20-JAN-2004; 2004US-00760752.
                                                                                                                                                                      12-MAR-2004; 2004US-00800161
                                                 (first entry)
                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                                 WPI; 2004-580223/56.
                                                                                                                              US2004154051-A1.
                                                  21-0CT-2004
                                                                                                                                                   05-AUG-2004
                              ADR16847;
                                                                                                                                                                                                                                                                                                                            interest
ADR16847
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The present invention relates to an Arabidopsis NII6 gene promoter useful in regulating transcription of coding sequence of interest. The invention is useful in production of transgenic plant or seed exhibiting resistance to herbicides and microorganism such as Phytophthora parasitica, pseudomonas syringae, Cercospora nicotianse, Peronospora parasitica. The

Claim 1; SEQ ID NO 28; 39pp; English.

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in regulating transcription of coding sequence of interest. The invention is useful in production of transgenic plant or seed exhibiting resistance to herbicides and microorganism such as Phytophthora parasitica. Pseudomonas syringae, Cercospora nicotianae, Peronospora parasitica. The present sequence is Arabidopsis thaliana NI16 promoter DNA. This sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                              GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTC 240
                                                                                                                                                                                                                                   ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGATGTCATTAGCAT 120
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                                                                                                                                                                            TCTAAAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                                                                                                                                                                                                                                                                                                     121 CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACGGTCTAAGTTCCACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NI16; transgenic; herbicide resistance; mouse-ear cress; promoter; ds
                                                                                                                                                                                                                                                                                                              CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
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                                                                           DB 13; Length 274;
                                                                                                                                                        1 TCTAGAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTT
                                  BP; 92 A; 58 C; 35 G; 89 T; 0 U; 0 Other;
is used in the exemplification of the invention
                                                                         Score 272.4; DB 1:
Pred. No. 1.4e-63;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rrgacraagcrraaacgacgccgrraacarrirc 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana NI16 promoter DNA #4.
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08-DEC-2000; 2000US-00733685.
20-JAN-2004; 2004US-00760752.
                                                                           99.48;
                                                                                           ilarity 99.6%;
Conservative
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                                                                                               Similarity
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                                      Sequence 274
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present sequence is Arabidopsis thaliana NI16 promoter DNA. This sequence
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                                                                                                                                                                                                                 rcragaaararagccgaraccaarrrrrccacacarggacrrccrrrarrccaaaagrca
                                                                                                                                                                                                                                                       ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT
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                                                                                                                                                                            TCTAGAAATATAGCCGATACCAATTTTTCCACACACAGGACTTCCTTTATTCCAAAAGTCA
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                                                                                               Length 274;
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                                                        Seguence 274 BP; 91 A; 58 C; 36 G; 89 T; 0 U; 0 Other;
                                                                                             Score 274; DB 13;
Pred. No. 5.2e-64;
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                      the exemplification of the invention.
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                                                                                                                                    0; Mismatches
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11-JAN-2000; 2000US-0175519P.
08-DEC-000; 2000US-0075052.
20-JAN-2004; 2004US-00760752.
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                                                                                                                                    274; Conservative
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                                                                                                               Similarity
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                                                                                               Query Match
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Sequence 862 BP; 337 A; 112 C; 152 G; 261 T; 0 U; 0 Other;
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                                      Matches 273;
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                                                                                                          ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120
                                                                                                                       240
                                                                                                                                                                                                           510
                                                                                      271 rcraaaaararagccgaraccaarrrrrccacacarggacrrccrrarrccaaagrca 330
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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule comprising Arabidopsis N116 promoter, useful in regulating transcription of coding sequence of
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                                DB 13; Length 544;
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             C; 95 G; 156 T; 0 U; 0 Other;
                              Score 272.4; DB 13;
Pred. No. 1.6e-63;
0; Mismatches 1;
                                                                                                                                                                                                                                          TTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana NI16 promoter DNA #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              claim 12; SEQ ID NO 25; 39pp; English.
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11-JAN-2000; 2000US-0175519P.
08-DEC-2000; 2000US-00733685.
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                               / Match
Local Similarity 99.6%;
hes 273; Conservative
               BP; 209 A; 84
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               Sequence 544
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                                                         1 TCTAGAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                Gaps
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707. .712
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/*tag= a
/mote= "This promoter is specifically claimed"
365. .374
Length 862;
                               1; Indels
DB 13;
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   Score 272.4; DB 1
Pred. No. 1.8e-63;
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/note= "HEXAMERAT ·4 element"
                                  0; Mismatches
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/note= "MYCATR22 element"
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/note= "TCAI motif"
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/note= "TCAI motif"
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/note= "PAL BOX"
757. .762
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11-JAN-2000; 2000US-0175519P.
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   99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .435
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                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                  Local Similarity
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in regulating transcription of coding sequence of interest. The invention is useful in production of transgenic plant or seed exhibiting resistance to herbicides and microorganism such as Phytophthora parasitica. Pseudomonas syringae, Cercospora nicotianae, Peronospora parasitica. The present sequence is Arabidopsis thaliana NI16 promoter DNA. This sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120
                                                                                                                                                                                                                                                                                                                                         present invention relates to an Arabidopsis NI16 gene promoter useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACGGCTATAAGAGTTTCATTATAAATTTTTAGCAAAATAAAATCAGCAAATAATTTTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TCTAGAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule comprising Arabidopsis NI16 promoter, useful in regulating transcription of coding sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NI16; SAR; systemic acquired resistance; mouse-ear cress; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 962 BP; 379 A; 125 C; 165 G; 293 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
99.4%; Score 272.4; DB 13; Length
Best Local Similarity 99.6%; Pred. No. 1.8e-63;
Matches 273; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ricaciaagciraaacgacgccgriaacarrirc 951
                                                                                                                                                                                                                                                                                                  Claim 11; SEQ ID NO 24; 39pp; English.
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/*tag= a
/note= "TCA1 motif"
/*tag= b
/note= "TCA1 motif"
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                                                                                                                                        Lawton KA;
                                                                                                   (SYGN ) SYNGENTA PARTICIPATIONS
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15-DEC-1999; 99US-0171008P.
11-JAN-2000; 2000US-0175519P.
08-DEC-2000; 2000US-00733685.
20-JAN-2004; 2004US-00760752.
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                                                                                                                                        Cade RM, Dietrich RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
                                                                                                                                                                              WPI; 2004-580223/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            원
                                                                                                                                                                                                                                                                                                The invention relates to a NI16 nucleic acid promoter sequence. The promoter sequence of the invention is useful for initiating transcription of DNA that encodes proteins involved in regulation of systemic acquired resistance (SAR) gene expression in plants. It enhances the expression of SAR genes such as pathogenesis related protein (PR-1), thus allows broadspectrum disease resistance in plant such as resistance against spectrum as syringae. The present sequence is the Arabidopsis thaliana NI16 gene including 5' upstream promoter. Note: This sequence is not given separately, but has been created from the NI16 gene (ADV66204) given in the sequence listing and the information provided in claim 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAAAGTGTGACGTCATGATACTTAACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACGGCTATAAGAGTTTCATTATAAATTTTTAGCAAAATAAAATCAGCAAATAATTTTTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTC 817
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                                                                                                                                                                              Novel isolated NI16 nucleic acid promoter, useful for initiating transcription of DNA that encodes proteins involved in regulation systemic acquired resistance (SAR) gene expression in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 272.4; DB 14; Length 862; Pred. No. 1.8e-63; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 862 BP; 337 A; 112 C; 152 G; 261 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana NI16 promoter DNA #1.
                                         (SYGN ) SYNGENTA PARTICIPATIONS AG.
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  08-DEC-2000; 2000US-00733685
                                                                                                                                                                                                                                                              Claim 1; Page; 32pp; English
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set Local Similarity 99.6%;
tches 273; Conservative
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                                                                                                                    WPI; 2005-020569/02.
P-PSDB; ADV66203.
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      ADR16822;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          817
                                                                                                                                                                                                                                               New NI16 nucleic acid sequence and encoded protein, useful for increasing systemic acquired resistance gene expression in a plant.
                                                                                                                                                                                                                                                                                                                                                                                               637
                                                                                                                                                                                                                                                                                                                                                                                                                              697
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                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to Arabidopsis NII6 gene encoding a protein involved in the regulation of SAR gene expression in plants. The NII6 muclecic acid molecule and the encoded protein is useful in increasing systemic acquired resistance (SAR) gene expression in a plant. The present sequence is Arabidopsis thaliana NII6 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                         CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
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                                     salicylic acid response element"
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0
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/product= "Arabidopsis thaliana NI16 protein"
                                                                                                                                                                                                                                                                                                                                   Sequence 1700 BP; 593 A; 237 C; 361 G; 509 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2e-63;
                                                                          /*tag= f
/note= "HEXAMERAT 4 element"
863. .1231
                                                                                                                                                                                                                                                                                                                                                 99.4%; Score 272.4;
99.6%; Pred. No. 2e-6
                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
        *tag= c
note= "MYCATR22 element"
                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 3; 29pp; English.
                                                                                                                                                                                            (SYGN ) SYNGENTA PARTICIPATIONS AG
                               *tag= d
note= "CAMV AS1
                                                     '*tag= e
'note= "PAL box"
                                                                                                                                                                     15-DEC-1999; 99US-0171008P.
                                                                                                                                                      08-DEC-2000; 2000US-00733685
                                            .712
                                                                  .762
 .614
                       .665
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Best Local Similarity 99.6
Matches 273; Conservative
                                                                                                                                                                                                           Dietrich RA;
                                                                                                                                                                                                                           WPI; 2004-313378/29.
                                                                                                                                                                                                                                  P-PSDB; ADN17258.
                                             misc_feature
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The present invention relates to an Arabidopsis NII6 gene promoter useful in regulating transcription of coding sequence of interest. The invention is useful in production of transgenic plant or seed exhibiting resistance to herbicides and microorganism such as Phytophthora parasitica. Pseudomonas syringae, Cercospora nicotianae, Peronospora parasitica. The present sequence is Arabidopsis thaliana NII6 genomic DNA, including the
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                                        NI16; transgenic; herbicide resistance; mouse-ear cress; ds; gene
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"CAMV AS1 salicylic acid response element"
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coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= g
/product= "Arabidopsis thaliana NI16 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule comprising promoter, useful in regulating transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "HEXAMERAT 4 element"
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/note= "MYCATR22 element"
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Arabidopsis thaliana NI16 genomic DNA
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/note= "TCAl motif"
126. .435
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                                                                                                                                            Location/Qualifiers
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/note= "TCA1 motif"
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/note= "PAL BOX'
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11-JAN-2000; 2000US-0175519P.
08-DEC-2000; 2000US-007368E.
20-JAN-2004; 2004US-00760752.
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Matches 273; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 757.
                                                                                                                                                                                                                                                426.
                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-580223/56.
P-PSDB; ADR16821.
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RESULT 8 ADR16822 ID ADR16822 standard; DNA; 1700 BP.

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The invention relates to a NII6 nucleic acid promoter sequence. The promoter sequence of the invention is useful for initiating transcription of DNA that encodes proteins involved in regulation of systemic acquired resistance (SAR) gene expression in plants. It enhances the expression of SAR genes such as pathogenesis-related protein (PR-1), thus allows broadspectrum disease resistance in plant such as resistance against Pseudomonas syringae. The present sequence is the Arabidopsis thaliana NII6 gene including 5' upstream promoter. Note: The promoter is specifically claimed in claim 1 - the isolated promoter is given in
                                                                                                                                                                                                                                                                                                                                                                                                                          61 ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTC 817
                                                                                                                                                                                                                                                                                                                                                                                         TCTAAAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                          CAATCTCCACCGTCCAATTTAATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTTC
                                                                                                                                                                                                                                                                                                                                                                         TCTAGAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                 Novel isolated NI16 nucleic acid promoter, useful for initiating transcription of DNA that encodes proteins involved in regulation of systemic acquired resistance (SAR) gene expression in plants.
                                                                                                                                                                                                                                                                                                                      DB 14; Length 1700;
                                                                                                                                                                                                                                                                                            Sequence 1700 BP; 593 A; 237 C; 361 G; 509 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rigaciaagciraaccaccccrraacarrirc 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic plant; NIMIN-2; expression; plant;
                                                                                                                                                                                                                                                                                                                                  Pred. No. 2e-63;
                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                      Score 272.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A. thaliana NIMIN-2 promoter SEQ ID NO:2.
                                                                                                                      Example 3; SEQ ID NO 3; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                    99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADW12661 standard; DNA; 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2003; 2003EP-00017114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.6
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYHO-) UNIV HOHENHEIM
    Dietrich RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                            2005-020569/02.
                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                          P-PSDB; ADV66203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1502953-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2003;
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    Cade RM,
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                                                                                                                                                                                                                                                                                                                      Query Match
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ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT
                                        ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTCATTAGCAT
                                                                                            CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
                                                                                                                   CAATCTCCACCGTCCAATTTAATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC
                                                                                                                                                GACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTC
                                                                                                                                                                        GACGCCTATAAGAGTTTCATTATAAATTTAGCAAAATAAAATCAGCAAATAATTTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                Systemic acquired resistance; disease-resistance; transgenic plant; plant; NI16; NIM1 interactor; gene; ds.
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note= "CAMV ASI salicylic acid response element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter is specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product= "Arabidopsis thaliana NI16 protein"
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                                                                                                                                                                                                                            ricaciaactraaaccaccccriaacarrirc 851
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note= "HEXAMERAT 4 element"
                                                                                                                                                                                                  TTGACTAAGCTTAAACGACGCCGTTAACATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "MYCATR22 element'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365. .374
/*tag= b
/note= "TCAI motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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note= "TCAI motif"
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                                                                                                                                                                                                                                                                                            ВР
                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana NI16 gene.
                                                                                                                                                                                                                                                                                            ADV66204 standard; DNA; 1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag≈ a
note= "This
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08-DEC-2000; 2000US-00733685
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/note= '
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                               24-FEB-2005
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                                                                                                                                                                                                                                                                                                                      ADV66204;
                                                                  638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
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New NI16 nucleic acid sequence and encoded protein, useful for increasing systemic acquired resistance gene expression in a plant.
                                                                                                                                                                                                                             The invention relates to Arabidopsis NI16 gene encoding a protein involved in the regulation of SAR gene expression in plants. The NI16 nucleic acid molecule and the encoded protein is useful in increasing systemic acquired resistance (SAR) gene expression in a plant. The present sequence is Arabidopsis thaliana NI16 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             219 AAAATCAGCAAATAATTTTTTTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid molecule comprising Arabidopsis N116 promoter, useful in regulating transcription of coding sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NI16; transgenic; herbicide resistance; mouse-ear cress; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "Arabidopsis thaliana NI16 protein"
                                                                                                                                                                                                                                                                                                                                    Sequence 509 BP; 158 A; 82 C; 133 G; 136 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                    19.3%; Score 52.8; DB 12; 96.4%; Pred. No. 0.00021; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 1; 39pp; English
                                                                                                                                                                                             Claim 2; SEQ ID NO 1; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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              (SYGN ) SYNGENTA PARTICIPATIONS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana NI16 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1999; 99US-0171008P.
11-JAN-2000; 2000US-017519P.
08-DEC-2000; 2000US-00733685.
20-JAN-2004; 2004US-00760752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-2004; 2004US-00800161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR16820 standard; cDNA; 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.43
Matches 54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dietrich RA,
                                                  Dietrich RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-580223/56.
                                                                                    WPI; 2004-313378/29
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                                                                                                        P-PSDB; ADN17258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cade RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interest
                                                Cad RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAAAGTGTGAGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGATGTCATTAGCAT 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel nucleic acid (I) containing at least a first nucleotide sequence chosen from a NIMIN-1 promoter sequence of (ADW12660) and NIMIN-2 promoter sequence of (ADW12661), and its biologically active derivative. The polymucleotide of the invention is useful in controlled expression of desired expression products in suitable host expression organisms such as transgenic plants. The present sequence represents the NIMIN-2 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACGCCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAATTTTTC 240
                                                                 Novel nucleic acid containing selectively inducible NIMIN-1 promoter sequence or NIMIN-2 promoter sequence, useful in controlled expression of desired expression products in suitable host expression organisms such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATAAAGTGTGACGTCATGATACTTACGCTTTAAAACATCGCATGATGATGTTAGCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTAGAAATATAGCCGATACCAATTTTTCCACACATGGACTTCCTTTATTCCAAAAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     systemic acquired resistance; mouse-ear cress; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                         Score 258.4; DB 14; Length 1226;
Pred. No. 1.1e-59;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Arabidopsis thaliana NI16 protein"
                                                                                                                                                                                                                                                                                                                                           Sequence 1226 BP; 496 A; 146 C; 201 G; 383 T; 0 U; 0 Other;
                                                                                                                                                               Claim 1; SEQ ID NO 2; 22pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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11-JAN-2000; 2000US-0175519P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN17257 Btandard; cDNA; 509
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Best Local Similarity 99.6%;
Matches 259; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
 Pfitzner A, Roth B;
                                   WPI; 2005-114423/13
                                                                                                                               transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NI16; SAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
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The invention relates to a NII6 nucleic acid promoter sequence. The promoter sequence of the invention is useful for initiating transcription of DNA that encodes proteins involved in regulation of systemic acquired resistance (SAR) gene expression in plants. It enhances the expression of SAR genes such as pathogenesis-related protein (PR-1), thus allows broad-spectrum disease resistance in plant such as resistance against
               in regulating transcription of coding sequence of interest. The invention is useful in production of transgenic plant or seed exhibiting resistance to herbicides and microorganism such as Phytophthora parasitica,
present invention relates to an Arabidopsis NI16 gene promoter useful
                                                             Pseudomonas syringae, Cercospora nicotianae, Peronospora parasitica. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas syringae. The present sequence is the Arabidopsis thaliana
NI16 cDNA obtained via a a NIM1 two-hybrid screen.
                                                                                                                                                                                                                 CTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                  AAAATCAGCAAATAAACTTTTCTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Systemic acquired resistance; disease-resistance; transgenic plant; plant; NI16; NIM1 interactor; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated NI16 nucleic acid promoter, useful for initiating transcription of DNA that encodes proteins involved in regulation systemic acquired resistance (SAR) gene expression in plants.
                                                                                                                                                                                  ;
0
                                                                                                                                                 Score 52.8; DB 13; Length 509;
Pred. No. 0.00021;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Arabidopsis thaliana NI16 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 509 BP; 158 A; 82 C; 133 G; 136 T; 0 U; 0 Other;
                                                                                                                 Sequence 509 BP; 158 A; 82 C; 133 G; 136 T; 0 U; 0 Other;
                                                                                present sequence is Arabidopsis thaliana NI16 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 1; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana NI16 cDNA.
                                                                                                                                                 19.3%;
                                                                                                                                                                                                                     AAAATCAGCAAATAATTTT
                                                                                                                                                                                                                                                                                                                                      ADV66202 standard; cDNA; 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JAN-2004; 2004US-00760752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0171008P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0175519P
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      od. .436
/*tag= a
                                                                                                                                                                                  54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cade RM, Dietrich RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2005-020569/02.
                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ADV66203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2004248303-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       24-FEB-2005
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                                                                                                                                                                                                                     219
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                                                                                                                                                                                                                                                                                                                                                                        ADV66202;
                                                                                                                                                  Query Match
                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                     RESULT 13
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DB 14; Length 509;

19.3%; Score 52.8;

Query Match

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The invention relates to a gene expression profile comprising one or more genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type of a a coronary artery endothellum, umbilical artery or vein endothellum, captic endothellum, dermal microvascular endothellum, pulmonary artery conductellum, manmary epithellum, prosette epithellum, pronchial epithellum, manmary epithellum, prosette cepithellum, renal epithellum, renal prothellum, renal epithellum, renal prothellum, renal epithellum, renal problast, pulmonary artery smooth cuscle, neonatal dermal fibroblast, pulmonary artery smooth muscle, dermal fibroblast, pulmonary artery smooth muscle, contic smooth muscle, mesangial cells, coronary artery smooth muscle, cortic smooth muscle, userine smooth muscle, astrocytes, costeoblasts or prostate stromal cells, coronary artery smooth muscle, costeoblasts or prostate stromal cells, coronary artery smooth muscle, costeoblasts are acal and distinguishing cell types. The gene expression profile is useful in identifying disease pathologies involving alterations of gene expression. The assessment of expression profiles may provide meaningful information with respect to tumour type and stage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment methods, and prognosis. The gene or protein expression profile may also be used for creating microarrays. The microarray is useful for genetic and physical mapping of genemes. DNA sequencing, genetic or medical diagnosis, genotyping of organisms, confirming cell or tissue identifications and in identifying promising antibiotics, antiviral or
                                                                                                                                                                                                                                                                                                                                                                             Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
gene expression; gene; ss.
                                                             219 AAAATCAGCAAATAATTTTTTTTTGACTAAGCTTAAACGACGCCGTTAACATTTTC 274
                        Gaps
                                                                                          1 AAAATCAGCAAATAAACTTTTCTTGACTAAAGCTTAAACGACGCGGTAAACATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New gene expression profile generated from primary, endothelial, epithelial, and muscle cell types, useful for identifying disease pathologies involving alterations of gene expression, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                          Human gene expression profile polynucleotide SEQ ID NO 676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 321;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 321 BP; 112 A; 51 C; 40 G; 113 T; 0 U; 5 Other;
  Pred. No. 0.00021;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.7%; Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 799; 850pp; English.
                                                                                                                                                                                                                 ABZ35565 standard; cDNA; 321 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2002; 2002WO-US008456.
96.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-2001; 2001US-0276947P
                                                                                                                                                                                                                                                                                                    (first entry)
                          54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-740862/80.
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antifungal agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200274979-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
                                                                                                                                                                                                                                                                                                    05-FEB-2003
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                                                                                                                                                                                                                                                             ABZ35565;
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                        Матсһев
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The invention comprises compositions used for the therapy and diagnosis of ovarian cancer. The compositions comprise one or more ovarian tumour proteins, their associated polymucleotides, or immunogenic portions of the proteins. The ovarian tumour polymucleotides and polypeptides are useful for stimulating and/or expanding T cells specific for a tumour protein. They are also useful for inhibiting the development of cancer in a patient with an ovarian tumour DNA or protein by incubating isolated T-cells allowing them to proliferate, and administering to the patient. The sequences can be used as markers for cancer, for example, to monitor ovarian cancer progression. Probes and primers are useful in nucleic acid hybridisation, in detecting the presence of complementary sequences in a given sample, for preparing mutant species and for preparing other genetic constructions. Sequences AASI31820-AASI2521 and AASI3182-AASIS539
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                                                    179
                                                                                                                      64 agaagactataagaaaacatattaatatataaaattaaaattaatacttcaaatacttra 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides encoding ovarian tumor proteins, useful for treating ovarian cancer, and as probes, primers, and markers of cancer
                                                                                    4 inanatriccarrigaaggrafiratriracagcrcarcrraagraagaaariccarac 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; 88;
gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
                                                    120 TCAATCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACAC
                  Gaps
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Best Local Similarity 56.7%; Pred. No. 0.085; Matches 76; Conservative 0; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ovarian PCR-subtracted cDNA library clone #1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 376; 378pp; English
                                                                                                                                                                                                                                                                                                                          AAS25538 standard; cDNA; 229 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000; 2000US-0180403P
28-MAR-2000; 2000US-0192745P
                                                                                                                                                                                                                        124 CATTANGATGATTA 137
                                                                                                                                                                                                240 CTTGACTAAGCTTA 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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15.3%; Score 42; DB 4; Length 229; 57.7%; Pred. No. 0.15; tive 0; Mismatches 55; Indels

Query Match 15.3 Best Local Similarity 57.7 Matches 75; Conservative

Sequence 229 BP; 96 A; 26 C; 33 G; 74 T; 0 U; 0 Other;

represent human ovarian tumour protein cDNA clones

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163 GACTATAACAGAAATCATATTTAATATTAAATTTAATACTTCAAATATCTTTCACATT 104
183
                          223 Triccarridaaggrafrafritarrificadcrcaficfraagracaaaarrccaracada 164
124 TCTCCACCGTCCAATTTATTTAGTTGTTGACAATATCGACCGTCTAAGTTCCACACCGAC
                                                                                                                         244 ACTAAGCTTA 253
                                                                                                                                                          103 AAGATGATTA 94
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